



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 190167

TO: Manjunath N Rao
Location: rem/2A01/2C70
Art Unit: 1652
Friday, May 19, 2006
Case Serial Number: 09/211691

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

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77025

mg

STIC-Biotech/ChemLib

190167

From: Chan, Christina
Sent: Tuesday, May 16, 2006 1:53 PM
To: Rao, Manjunath N.; STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search request for 09/211691

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
MAY 16 2006
STIC/CHEN, C. Chan
(STIC)

-----Original Message-----

From: Rao, Manjunath N.
Sent: Tuesday, May 16, 2006 1:50 PM
To: Chan, Christina
Subject: RUSH sequence search request for 09/211691

Hello Christina,

Please authorize the request below as RUSH. The reason being, this is an RCE and applicants have now included the following sequences in their claims.

Many Thanks
-Manjunath

Manjunath N. Rao
Art Unit 1652, Room 2A01,
Mail Box in Room 2C70,
Remsen Building, USPTO
400, Dulany St.
Alexandria, VA.
Phone: 571-272-0939

From: Manjunath N. Rao
Art Unit 1652, Room 2A01
Mail Box in Room 2C70
Phone: 272-0939

Date: 5-16-06

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Please search the following as soon as possible for application with serial number
09/211691

1. SEQ ID NO: 5 and 6 against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results

If you have any questions please call me at the above phone number.

Thanks

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 00:44:40 ; Search time 789.333 Seconds

(without alignments)
2997.535 Million cell updates/sec

Title: US-09-211-691-5

Perfect score: 37

Sequence: 1 gcacgaatctgcggctgaagaagctcttgcacc 37

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl1:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hlg:*
13: gb_in:*
14: gb_cm:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	26.4	71.4	2039	15 NMU060660	U60660 Neisseria m
2	26.4	71.4	110000	15 AE002098_09	Continuation (10 o
3	26.4	71.4	331801	15 NMA422491	AL162755 Neisseria
4	26.4	71.4	349980	2 CS238429	CS238429 Sequence
5	26.4	71.4	349980	2 CS238430	CS238430 Sequence
6	26.4	71.4	349980	2 AX044030	AX044030 Sequence
7	26.4	71.4	349980	2 AX044031	AX044031 Sequence
8	26.4	70.3	1116	2 ARI05309	ARI05309 Sequence
9	26.4	70.3	1116	2 ARI144756	ARI144756 Sequence
10	26.4	70.3	1116	2 BD009732	BD009732 Recombina
11	26.4	70.3	1116	2 NMU06061	U60661 Neisseria m
12	26.4	70.3	1116	15 NMU06062	U60662 Neisseria m
13	26.4	65.9	110000	15 NMU06063	U60663 Neisseria m
14	26.4	65.9	110000	4 AP008212_046	Continuation (47 o
15	26.4	65.9	110000	4 AP008210_235	Continuation (236
16	26.4	65.9	110000	4 AP008211_091	Continuation (92 o
17	26.4	65.9	110000	4 AP008211_092	Continuation (93 o
18	26.4	65.9	139298	4 OSJN00012	AT606441 Oryza sat

C 19	24.4	65.9	164925	4 AC121362	AC121362 Oryza sat
C 20	24.4	65.9	174500	4 AP004738	AP004738 Oryza sat
C 21	23.8	64.3	110000	12 CR382382_2	Continuation (3 of
C 22	23.8	64.3	179667	12 CR854852	CR854852 Danio rer
C 23	23.8	64.3	191778	12 CR856633	CR856633 Danio rer
C 24	23.8	64.3	197593	12 CR855360	CR855360 Danio rer
C 25	23.8	64.3	215198	6 AC113180	AC113180 Mus muscu
C 26	23.8	64.3	227326	12 CR854836	CR854836 Danio rer
C 27	23.8	64.3	231100	11 AL954512	AL954512 Zebrafish
C 28	23.8	64.3	256720	6 AC110241	AC110241 Mus muscu
C 29	23.6	63.8	726	2 BD149112	BD149112 Primer fo
C 30	23.6	63.8	726	2 AX869050	AX869050 Sequence
C 31	23.4	63.2	425	5 AY859405	AY859405 Macaca mu
C 32	23.4	63.2	80050	5 AC124833	AC124833 Homo sapi
C 33	23.4	63.2	178555	12 AC027397	AC027397 Homo sapi
C 34	23.2	62.7	2613	2 CQ598079	CQ598079 Sequence
C 35	23.2	62.7	5356	10 AB069671	AB069671 Crimaean-C
C 36	23.2	62.7	5356	10 AB069672	AB069672 Crimaean-C
C 37	23.2	62.7	5356	10 AY234476	AY234476 Crimaean-C
C 38	23.2	62.7	57335	12 AC015272	AC015272 Drosophila
C 39	23.2	62.7	188459	13 AC008312	AC008312 Drosophila
C 40	23.2	62.7	197597	13 AC011253	AC011253 Drosophila
C 41	23.2	62.7	315844	13 AE003671	AE003671 Drosophila
C 42	23	62.2	1359	2 CQ734837	CQ734837 Sequence
C 43	23	62.2	1734	2 AR578067	AR578067 Sequence
C 44	23	62.2	2161	5 BC032942	BC032942 Homo sapi
C 45	23	62.2	2228	2 BD158353	BD158353 Primer to

ALIGNMENTS

RESULT 1	NMU06060	2039 bp	DNA	linear	BCF 08-NOV-1996
LOCUS	Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete cds, and isocitrate dehydrogenase and cytochrome c genes, partial				
DEFINITION	Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete cds, and isocitrate dehydrogenase and cytochrome c genes, partial				
ACCESSION	U60660				
VERSION	U60660.1	GI:1546002			
KEYWORDS	Neisseria meningitidis				
SOURCE	Neisseria meningitidis				
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.				
REFERENCE	1 (bases 1 to 2039)				
AUTHORS	Gilbert M., Watson D.C., Cunningham A.M., Jennings M.P., Young N.M. and Wakarchuk W.W.				
TITLE	Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from the bacterial pathogen Neisseria meningitidis and Neisseria gonorrhoeae				
JOURNAL	J. Biol. Chem. 271 (45), 28271-28276 (1996)				
PUBMED	8910446				
REFERENCE	2 (bases 1 to 2039)				
AUTHORS	Gilbert M., Michniewicz J.J., Watson D.C. and Wakarchuk W.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-JUN-1996) Institute for Biological Sciences, National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada				
FEATURES	location/Qualifiers				
source	1..2039				
	/organism="Neisseria meningitidis"				
	/mol_type="genomic DNA"				
	/strain="MC58, NRC 4728"				
	/db_xref="taxon:487"				
	/note="lipooligosaccharide type: L3"				
	complement(1..140)				
	/note="similar to isocitrate dehydrogenase from Azotobacter vinelandii"				
	/codon_start=1				
	/transl_table=11				
	/product="isocitrate dehydrogenase"				
	/protein_id="AAC44540.1"				

CDS

/db_xref="GI:1546003"
 /translation="MTQKSTIVYHTDEAPALATQSLPIVQAFARHADIVTSDIS
 LSG".1688
 /note="Expression and functionality of the product were
 both determined experimentally"
 /codon_start=1
 /transl_table=1
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 /protein_id="AAC44541.1"
 /db_xref="GI:1546004"
 /translation="MGKKAQCLVLCIVCEGPIPTFDRVNOGERNVSLKEKLFN
 EEKPVNLIKCYTTLQMKVABRIMAQHPSGRFYVLMSENREKDYVFNQIDKAE
 AYFPHLYGLKSNFNPITVAELKVKSMLEPKVRIYLALEKVSIAFLSTYPAEI
 KTFDGTGNLIQSSSYGDEFSVNGITKRNFAFMIMIGWSIAKTRNASDEHTIFKGL
 KNIMDDGRKMTYLPFDASELKTGDEGTGTVRIILGSPDKEMKEISEKAANKFIQY
 VAPHRQTJSGVTLNTPYVIEDYILREIKNPHRYEITTFPGSALITMKDFPNV
 HVYALKPASIPEDYWLKPYVALPTQSGIPILTFDDKN"
 complement(1653..2039)
 /note="similar to cytochrome c' from Rhodopseudomonas
 gelatinosa"
 /codon_start=2
 /transl_table=11
 /product="Cytochrome c'"
 /protein_id="AAC44542.1"
 /db_xref="GI:1546005"
 /translation="RALPRAWSDGAKFEAKTKFAAAVEKLNAAAQTGLDEIKAYG
 ETGASCSCSDSRAPR"

ORIGIN

Query Match 71.4%; Score 26.4; DB 15; Length 2039;
 Best Local Similarity 96.4%; Pred. No. 1.2;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGGCTTGAAAAAGCCTTGTGACC 37
 |||||
 Db 572 TATGGGCTTGAAAAAGCCTTGTGACC 599

RESULT 2
 AE002098_09
 WPCOMMENT
 Sequence split into 23 fragments LOCUS AE002098 Accession AE002098

Fragment Name	Begin	End
AE002098_00	1	110000
AE002098_01	100001	210000
AE002098_02	200001	310000
AE002098_03	300001	410000
AE002098_04	400001	510000
AE002098_05	500001	610000
AE002098_06	600001	710000
AE002098_07	700001	810000
AE002098_08	800001	910000
AE002098_09	900001	1010000
AE002098_10	1000001	1110000
AE002098_11	1100001	1210000
AE002098_12	1200001	1310000
AE002098_13	1300001	1410000
AE002098_14	1400001	1510000
AE002098_15	1500001	1610000
AE002098_16	1600001	1710000
AE002098_17	1700001	1810000
AE002098_18	1800001	1910000
AE002098_19	1900001	2010000
AE002098_20	2000001	2110000
AE002098_21	2100001	2210000
AE002098_22	2200001	2272360

Continuation (10 of 23) of AE002098 from base 900001 (AE002098 Neisseria meningitidis MG
 Query Match 71.4%; Score 26.4; DB 15; Length 110000;
 Best Local Similarity 96.4%; Pred. No. 0.66;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGGCTTGAAAAAGCCTTGTGACC 37
 |||||
 Db 34787 TATGGGCTTGAAAAAGCCTTGTGACC 34814

RESULT 3
 NMA42491
 LOCUS
 DEFINITION
 Neisseria meningitidis serogroup A strain Z2491 complete genome;
 segment 4/7.
 AL162755 AL162755.2 GI:7379742

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
 Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
 Davies,R.M., Davis,P., Devlin,K., Felwell,T., Hamlin,N.,
 Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,
 Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
 Skellon,J., Whitehead,S., Spratt,B.G. and Barrall,B.G.
 Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis Z2491
 Nature 404 (6777), 502-506 (2000)
 10761919

REFERENCE
 PUBMED
 Parkhill,J.
 Direct Submission
 Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
 sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
 Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

COMMENTS
 Details of N. meningitidis sequencing at the Sanger Centre are
 available on the World Wide Web.
 (URL: http://www.sanger.ac.uk/Projects/N_meningitidis/).
 Location/Qualifiers
 1..331801
 /organism="Neisseria meningitidis Z2491"
 /mol_type="genomic DNA"
 /strain="Z2491"
 /db_xref="taxon:122567"
 /note="serogroup: A"
 117..1333
 /gene="NMA1040"
 /pseudo
 117..1333
 /gene="NMA1040"
 /note="NMA1040, possible type I restriction-modification
 system specificity protein, pseudogene, len. 1217 bp;
 N-terminus shows weak similarity to the C-terminal half of
 TR:Q0359 (EMBL:L25415), hsdS1B, Mycoplasma pulmonis
 restriction-modification enzyme subunit S1B (335 aa),
 fasta scores: E(): 2.3e-06, 26.2% identity in 141 aa,
 overlap and to many hypothetical restriction-modification
 subunits. Also similar to NMA1041, fasta scores: E():
 4.8e-10, 37.0% identity in 100 aa overlap. C-terminus
 similar to part of SW:TI51.EC01 (EMBL:X13145), hsdS,
 Escherichia coli type I restriction enzyme Ecor1241
 specificity protein (410 aa), fasta scores: E(): 1.9e-14,
 39.6% identity in 182 aa overlap. Similar to NMA1040.E():
 2.9e-09, 38.0% identity in 100 aa overlap. Contains Pfam
 match to entry PF01420 Methylase_S, Type I restriction
 modification DNA specificity domain. Contains a G(8) tract
 which would allow translation as an intact CDS, if
 variable. Lies within a region of unusually low GC
 content."
 /pseudo
 /codon_start=1
 /transl_table=11
 /product="pseudogene (putative type I

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misc_feature      complement(157. .166)
                  /note="Core DNA uptake sequence: gccgctcgaa"
                  /label=DUS
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                  /note="Pfam match to entry PF01420 Methylase_S, Type I
                  restriction modification DNA specificity domain, score
                  105.50, E-value 1.1e-27"
                  /pseudo
repeat_region     699. .706
                  /note="(g)8"
                  726. .735
misc_feature      /gene="NMA1040"
                  /note="Core DNA uptake sequence: gccgctcgaa"
                  /pseudo
                  /label=DUS
                  740. .1231
misc_feature      /gene="NMA1040"
                  /note="Pfam match to entry PF01420 Methylase_S, Type I
                  restriction modification DNA specificity domain, score
                  158.70, E-value 1e-43"
                  /pseudo
RBS               1405. .1408
                  1415. .4509
gene              /gene="NMA1042"
                  /pseudo
                  1415. .4509
CDS               /gene="NMA1042"
                  /note="NMA1042", pseudogene, probable type I
                  restriction-modification system restriction protein, len:
                  291 aa, similar to parts of many e.g. SW:TRK1_ECOLI
                  (EMBL:U13145), hsdR, Escherichia coli type I restriction
                  enzyme EcoRI2411 R protein (EC 3.1.21.3) (1033 aa), fasta
                  scores: E(): 0, 73.9% identity in 291 aa overlap (frame
                  1), followed by a stop codon, E(): 0, 92.9% identity in
                  127 aa overlap (frame 1), followed by a frameshift near a
                  poly-A tract, E(): 0, 72.5% identity in 604 aa overlap
                  (frame 3)"
                  /pseudo
                  /codon_start=1
                  /transl_table=11
                  /product="type I restriction-modification system
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misc_feature      /note="Core DNA uptake sequence: gccgctcgaa"
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                  /note="Core DNA uptake sequence: gccgctcgaa"
                  /pseudo
                  /label=DUS
                  1761. .1770
misc_feature      /gene="NMA1042"
                  /note="Core DNA uptake sequence: gccgctcgaa"
                  /pseudo
                  /label=DUS
                  3906. .3915
misc_feature      /gene="NMA1042"
                  /note="Core DNA uptake sequence: gccgctcgaa"
                  /pseudo
                  /label=DUS
stem_loop         4514. .4545
                  /note="Stem loop containing DNA uptake sequences: aaaa
                  gccgctcgaa at ttcagacgc atttc"
                  4519. .4528
misc_feature      /note="Core DNA uptake sequence: gccgctcgaa"
                  /label=DUS
                  complement(4531. .4540)
misc_feature      /note="Core DNA uptake sequence: gccgctcgaa"
                  /label=DUS
                  complement(4559. .6838)
gene              /gene="cIpa"

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CDS               complement(4559. .6838)
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                  /note="NMA1045, cIpa, probable ATP-dependent protease
                  ATP-binding protein, len: 759 aa, similar to many e.g.
                  SW:CLPA_ECOLI (EMBL:M31045), cIpa, Escherichia coli
                  ATP-dependent CIP protease ATP-binding subunit (758 aa),
                  fasta scores: E(): 0, 56.2% identity in 762 aa overlap,
                  similar to NMA1683, fasta scores: E(): 0, 37.2% identity
                  in 844 aa overlap. Contains Pfam match to entry PF00495
                  cIpa_B, Chaperonin cIpa/B, PS00870 Chaperonins cIpa/B
                  signature 1, PS00871 Chaperonins cIpa/B signature 2 and
                  two PS00017 ATP/GTP-binding site motif A (P-loop)"
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                  /transl_table=11
                  /product="putative ATP-dependent protease ATP-binding
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                  /protein_id="CAB84311.1"
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                  /db_xref="InterPro:IPR001270"
                  /db_xref="InterPro:IPR003593"
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                  /db_xref="InterPro:IPR004176"
                  /db_xref="UniProtKB/TrEMBL:O94V15"
                  /translation="MSPLEHITLQIYREARARVETSLHLIVLIEEDAAVNV
                  LKICGADLKYSQQLAASVAENTPQIPDHLIDIVETOPTIGFPRVIGRAMVHTOSACK
                  AAVEPDILVAMSSSESHAVYFLKQSLITREVLICLAGSPDEEDGNSDGLRG
                  EBAEQGTGSLSDYVNLNMEVKAGRIDPLRGHEMERLQIICRRKNPDLVGEAG
                  VGTALAEGLAQIVKGDIPDALDAEVAIADMGSLAGIKRYGDFEAPRVKSVLKQLE
                  IKHALIFDEIHITIGAGSTSGTGDASNLALPALAKGRLRGATGYEVRIYFQK
                  DHASRRPKDIVPEPTVETVOILGKIMFEGFPQVRYTGQALEAALSAKYINE
                  RLPDPAIDMDAGAAQRILPSSKOKYIKQAQIETVIAKARVIREKTYSHDDKYL
                  QIFGRRLKNNVQDENAIYALVAVMSSSGELPKPKISFLPSGTGKVEAQ
                  LASMGPVLPQRPMSYMERHVAVRIGAPGVYGEQGLTEAVNKKOPCVLLDE
                  IEKAHPDIFNVLLQVMDAGKLTNNKSKADPFRVILIMTNAGAESLSRPSLFTAK
                  ERGDEQAINKLFTEPFRRRLDAIIFAPLSEDIIVKVDKFLQJLEHRLDDKVEAE
                  FPAALRKLYAEKGFDPOMGARPMNRILQEKIRKRLADELLFGLTVGGFPRIDMDAK
                  EBAVLKFKSKVPEETETV"
                  complement(4637. .5578)
                  /gene="cIpa"
                  /note="Pfam match to entry PF00495 cIpa_B, Chaperonin
                  cIpa/B, score 583.70, E-value 1.1e-171"
                  complement(5228. .5284)
                  /gene="cIpa"
                  /note="PS00871 Chaperonins cIpa/B signature 2"
                  complement(5330. .5353)
                  /gene="cIpa"
                  /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                  complement(5894. .5932)
                  /gene="cIpa"
                  /note="PS00870 Chaperonins cIpa/B signature 1"
                  complement(6173. .6196)
                  /gene="cIpa"
                  /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                  6374. .6383
misc_feature      /note="Core DNA uptake sequence: gccgctcgaa"
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                  complement(6842. .7153)
gene              /gene="NMA1046"
                  complement(6842. .7153)
CDS               /gene="NMA1046"

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Query Match      71.4%; Score 26.4; DB 15; Length 331801;
Best Local Similarity 96.4%; Pred. No. 0.78;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGGCTTGAAGAGCTGTTGACC 37
DB 67456 TATGGGCTTGAAGAGCTGTTGACC 67483

RESULT 4
CS238429

```

LOCUS	CS238429	349980 bp	DNA	linear	PAT 04-JAN-2006
DEFINITION	Sequence 111 from Patent EP1605061.				
ACCESSION	CS238429				
VERSION	CS238429.1	GI:84364856			
KEYWORDS					
SOURCE					
ORGANISM	Neisseria meningitidis				
REFERENCE	Neisseria meningitidis				
AUTHORS	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
JOURNAL	Neisseriaceae; Neisseria.				
FEATURES	1				
source	Pizza, M. Patent: EP 1605061-A 111 14-DEC-2005; CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US) Location/Qualifiers 1..349980 /organism="Neisseria meningitidis" /mol_type="unassigned DNA" /db_xref="taxon:487" /note="seq 1 to long, 2242716 replaced by new seq 1, from 1 to 349980 seq 110, from 300001 to 649980 seq 111, from 600001 to 949980 seq 112, from 900001 to 1249980 seq 113, from 1200001 to 1549980 seq 114, from 1500001 to 1849980 seq 115, from 1800001 to 2149980 seq 116, from 2100001 to 2242716"				
ORIGIN					
Query Match	71.4%; Score 26.4; DB 2; Length 349980;				
Best Local Similarity	96.4%; Pred. No. 0.78;				
Matches	27; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
QY	10 TCTGGCTGAAAGCGTTGTTGACC 37				
DB	334750 TATGGCTTGAAAAAGCGTTGTTGACC 334777				
RESULT 5					
LOCUS	CS238430	349980 bp	DNA	linear	PAT 04-JAN-2006
DEFINITION	Sequence 112 from Patent EP1605061.				
ACCESSION	CS238430				
VERSION	CS238430.1	GI:84364857			
KEYWORDS					
SOURCE					
ORGANISM	Neisseria meningitidis				
REFERENCE	Neisseria meningitidis				
AUTHORS	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
JOURNAL	Neisseriaceae; Neisseria.				
FEATURES	1				
source	Pizza, M. Patent: EP 1605061-A 112 14-DEC-2005; CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US) Location/Qualifiers 1..349980 /organism="Neisseria meningitidis" /mol_type="unassigned DNA" /db_xref="taxon:487" /note="seq 1 to long, 2242716 replaced by new seq 1, from 1 to 349980 seq 110, from 300001 to 649980 seq 111, from 600001 to 949980 seq 112, from 900001 to 1249980 seq 113, from 1200001 to 1549980 seq 114, from 1500001 to 1849980 seq 115, from 1800001 to 2149980 seq 116, from 2100001 to 2242716"				
ORIGIN					
Query Match	71.4%; Score 26.4; DB 2; Length 349980;				
Best Local Similarity	96.4%; Pred. No. 0.78;				
Matches	27; Conservative	0; Mismatches	1; Indels	0; Gaps	0;

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Qy      Db      34750  TATGGGCTTGAAGGCTTTGTACC 34777

RESULT 6    AX044030          349980 bp       DNA        linear   PAT 24-NOV-2000
LOCUS      AX044030
DEFINITION Sequence 109 from Patent WO0066791.
ACCESSION  AX044030
VERSION     AX044030.1 GI:11342914
KEYWORDS
SOURCE      Neisseria meningitidis
ORGANISM    Neisseria meningitidis
            Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
            Neisseriaceae; Neisseria.
REFERENCE   1
AUTHORS     Pizza,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C.,
            Maignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M.,
            Scarlato,V., Rappunli,R., Frazer,C.M. and Grandi G.
TITLE       Neisseria genomic sequences and methods of their use
JOURNAL     Patent: WO 006791-A 109 09-NOV-2000;
FEATURES
Source      CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
            Location/Qualifiers
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               /organism="Neisseria meningitidis"
               /mol_type="unassigned DNA"
               /db_xref="taxon:487"
             /note="sequence too long, cut in 8 pieces."
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             seq 108: 30001 to 64980 349980 bases
             seq 109: 60001 to 94980 349980 bases
             seq 110: 90001 to 124980 349980 bases
             seq 111: 120001 to 154980 349980 bases
             seq 112: 150001 to 184980 349980 bases
             seq 113: 180001 to 214980 349980 bases
             seq 114: 210001 to 2272325 172325 bases"

ORIGIN
Query Match 71.4%; Score 26.4; DB 2; Length 349980;
Best Local Similarity 96.4%; Pred. No. 0.78;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      Db      334749  TATGGGCTTGAAGGCTTTGTACC 334776

RESULT 7    AX044031          349980 bp       DNA        linear   PAT 24-NOV-2000
LOCUS      AX044031
DEFINITION Sequence 110 from Patent WO0066791.
ACCESSION  AX044031
VERSION     AX044031.1 GI:11342915
KEYWORDS
SOURCE      Neisseria meningitidis
ORGANISM    Neisseria meningitidis
            Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
            Neisseriaceae; Neisseria.
REFERENCE   1
AUTHORS     Pizza,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C.,
            Maignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M.,
            Scarlato,V., Rappunli,R., Frazer,C.M. and Grandi G.
TITLE       Neisseria genomic sequences and methods of their use
JOURNAL     Patent: WO 006791-A 110 09-NOV-2000;
FEATURES
Source      CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
            Location/Qualifiers
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               /mol_type="unassigned DNA"
               /db_xref="taxon:487"
             /note="sequence too long, cut in 8 pieces."
             seq 1: 1 to 349980 349980 bases

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seq 108: 300001 to 649980 349980 bases
seq 109: 600001 to 949980 349980 bases
seq 110: 900001 to 124980 349980 bases
seq 111: 120001 to 154980 349980 bases
seq 112: 150001 to 184980 349980 bases
seq 113: 180001 to 214980 349980 bases
seq 114: 210001 to 2272325 172325 bases"

ORIGIN

Query Match 71.4%; Score 26.4; DB 2; Length 349980;
Best Local Similarity 96.4%; Pred. No. 0.78;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TCTGGCTTGAAGGCTTTTGACC 37
Db 34749 TATGGCTTGAAGGCTTTTGACC 34776

RESULT 8
ARI05309
LOCUS ARI05309 1116 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6096529.
ACCESSION ARI05309
VERSION ARI05309.1 GI:12818906
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P.
TITLE Recombinant alpha-2,3-sialyltransferases and their uses
JOURNAL Patent: US 6096529-A 1 01-AUG-2000;
FEATURES
source Location/Qualifiers
1..1116
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 70.3%; Score 26; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGGCTTGAAGGCTTTTGACC 37
Db 2 TGGGCTTGAAGGCTTTTGACC 27

RESULT 9
ARI44756
LOCUS ARI44756 1116 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210933.
ACCESSION ARI44756
VERSION ARI44756.1 GI:15106623
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P. and
Moxon,E.Richard.
TITLE Recombinant alpha-2,3-sialyltransferases and their uses
JOURNAL Patent: US 6210933-A 1 03-APR-2001;
FEATURES
source Location/Qualifiers
1..1116
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 70.3%; Score 26; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGGCTTGAAGGCTTTTGACC 37

Db 2 TGGGCTTGAAGGCTTTTGACC 27

RESULT 10
BD009732
LOCUS BD009732 1116 bp DNA linear PAT 31-JAN-2002
DEFINITION Recombinant alpha-2,3-sialyltransferases and their uses.
ACCESSION BD009732
VERSION BD009732.1 GI:18638105
KEYWORDS JP 2001503961-A/1.
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 1116)
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P.
TITLE Recombinant alpha-2,3-sialyltransferases and their uses
JOURNAL Patent: JP 2001503961-A 1 27-MAR-2001;
COMMENT NATIONAL RESEARCH COUNCIL OF CANADA
OS Neisseria meningitidis
PN JP 2001503961-A/1
PD 27-MAR-2001
PF 10-JUN-1997 JP 1997526320
PR MICHEL GILBERT,WARREN W WAKARCHUK,MARTIN N YOUNG, PI MICHAEL P JENNINGS
PC C12N15/54,C12N15/70,C12N15/79,C12N9/10,C12N5/10,C12N1/21, PC
C12P19/26
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 1..1116
Location/Qualifiers
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/organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/db_xref="taxon:487"

ORIGIN

Query Match 70.3%; Score 26; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGGGCTTGAAGGCTTTTGACC 37
Db 2 TGGGCTTGAAGGCTTTTGACC 27

RESULT 11
NMU60661
LOCUS NMU60661 1116 bp DNA linear BCT 08-NOV-1996
DEFINITION Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete
cgs.
ACCESSION U60661
VERSION U60661.1 GI:1546006
KEYWORDS
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 1116)
AUTHORS Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,M.N.
and Wakarchuk,W.W.
TITLE Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from
the bacterial pathogens Neisseria meningitidis and Neisseria
gonorrhoeae
JOURNAL J. Biol. Chem. 271 (45), 28271-28276 (1996)
PUBMED 8910446
REFERENCE 2 (bases 1 to 1116)
AUTHORS Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-1996) Institute for Biological Sciences, National

Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada

Location/Qualifiers

1. .1116

/organism="Neisseria meningitidis"

/mol_type="genomic DNA"

/strain="406Y, NRCC 4030"

/db_xref="taxon:487"

/note="Capsule type: Y; lipooligosaccharide type: L3"

1. .1116

/note="The gene product activity was determined experimentally"

/codon_start=1

/transl_table=11

/product="alpha-2,3-sialyltransferase"

/protein_id="AAC44543.1"

/db_xref="GI:1546007"

/translation="MGKKKACLVLCIVFCGIFFTPDNRVNHGERRNAVSLDKLFLN EEEBPVNLIFCYTILQMKVARIQAQHPGERFYVVLMSERNREKDYDFYKQIKDAER AVEFHLPGYGNKSFNFIPYMAELKVKSMLEPKRYIASLEKVSIAAFISTYPAEI KTFDDGTGNLIQSSSYLGDEFVNGTIRKRFAMMIGDMSIAKTRNASDEHYTIFRGL KNIMDDGRKMTYLPFLFDSSELKAGDEGTGTVILIGSPDKEMKEISEKAANKFNIOY VAPHPROTGLSGVTTNSPYVEDIILREIKKNPHTREIYTFPSGALITMKDFPNV HYALAKPASLPEDYWLKPYVALFTQSGIPILTFDDKN"

ORIGIN

Query Match 70.3%; Score 26; DB 15; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAAAAGCCTGTTTGACC 37
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2 TGGGCTTGAAAAAGCCTGTTTGACC 27
|||||

RESULT 12
NMU60662 1116 bp DNA linear BCT 13-DEC-1999
LOCUS Neisseria meningitidis alpha-2,3-sialyltransferase gene, complete cds.
VERSION U60662.2 GI:6563405
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 1116)
Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,N.M. and Wakarchuk,W.W.
Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from the bacterial pathogens Neisseria meningitidis and Neisseria gonorrhoeae
J. Biol. Chem. 271 (45), 28271-28276 (1996)
8910446

REFERENCE
PUBMED 2 (bases 1 to 1116)
AUTHORS Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.
TITLE Direct Submission
JOURNAL Submitted (13-0UN-1996) Institute for Biological Sciences, National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada
3 (bases 1 to 1116)
Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1999) Institute for Biological Sciences, National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada

REMARK
COMMENT Sequence update by submitter
FEATURES
On Dec 13, 1999 this sequence version replaced gi:1546008.
1. .1116
Location/Qualifiers
/organism="Neisseria meningitidis"
/mol_type="genomic DNA"

Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada

Location/Qualifiers

1. .1116

/organism="Neisseria meningitidis"

/mol_type="genomic DNA"

/strain="M982B, NRCC 4725"

/db_xref="taxon:487"

/note="lipooligosaccharide type: L7"

1. .456

/note="This gene encodes an inactive truncated version of the alpha-2,3-sialyltransferase"

/codon_start=1

/transl_table=11

/product="alpha-2,3-sialyltransferase"

/protein_id="AAC44545.1"

/db_xref="GI:1546011"

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ORIGIN

Query Match 70.3%; Score 26; DB 15; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAAAAGCCTGTTTGACC 37
|||||
2 TGGGCTTGAAAAAGCCTGTTTGACC 27
|||||

RESULT 13
NMU60663 1115 bp DNA linear BCT 08-NOV-1996
LOCUS Neisseria meningitidis truncated alpha-2,3-sialyltransferase gene, complete cds.
VERSION U60663.1 GI:1546010
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 1115)
Gilbert,M., Watson,D.C., Cunningham,A.M., Jennings,M.P., Young,N.M. and Wakarchuk,W.W.
Cloning of the lipooligosaccharide alpha-2,3-sialyltransferase from the bacterial pathogens Neisseria meningitidis and Neisseria gonorrhoeae
J. Biol. Chem. 271 (45), 28271-28276 (1996)
8910446

REFERENCE
PUBMED 2 (bases 1 to 1115)
AUTHORS Gilbert,M., Michniewicz,J.J., Watson,D.C. and Wakarchuk,W.W.
TITLE Direct Submission
JOURNAL Submitted (13-0UN-1996) Institute for Biological Sciences, National Research Council of Canada, 100 Sussex Drive, Ottawa, Ontario K1A 0R6, Canada

FEATURES
source
1. .1115
Location/Qualifiers
/organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/strain="M982B, NRCC 4725"
/db_xref="taxon:487"
/note="lipooligosaccharide type: L7"
1. .456
/note="This gene encodes an inactive truncated version of the alpha-2,3-sialyltransferase"

ORIGIN

Query Match 65.9%; Score 24.4; DB 15; Length 1115;
Best Local Similarity 96.2%; Pred. No. 10;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 12 TGGGCTGAAAAGCTGTTGACC 37
Db 2 TGAGCTGAAAAGCTGTTGACC 27

RESULT 14
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WPCOMMENT

Sequence split into 308 fragments LOCUS AP008212 Accession AP008212

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AP008212_003	300001	410000
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AP008212_008	800001	910000
AP008212_009	900001	1010000
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AP008212_011	1100001	1210000
AP008212_012	1200001	1310000
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AP008212_014	1400001	1510000
AP008212_015	1500001	1610000
AP008212_016	1600001	1710000
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AP008212_027	2700001	2810000
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AP008212_030	3000001	3110000
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Query Match 65.9%; Score 24.4; DB 4; Length 110000;
Best Local Similarity 82.4%; Pred. No. 7;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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4 TGAATTCGGGCTTGAAGGCTTGTGACC 37

DB 16436 TGAATGCAGACTTGAAGGCTTGTGACC 16403

RESULT 15
AP008210_235/c
WPCOMMENT

Sequence split into 355 fragments LOCUS AP008210 Accession AP008210

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AP008210_014	1400001	151000
AP008210_015	1500001	161000
AP008210_016	1600001	171000
AP008210_017	1700001	181000
AP008210_018	1800001	191000
AP008210_019	1900001	201000
AP008210_020	2000001	211000
AP008210_021	2100001	221000
AP008210_022	2200001	231000
AP008210_023	2300001	241000
AP008210_024	2400001	251000
AP008210_025	2500001	261000
AP008210_026	2600001	271000
AP008210_027	2700001	281000
AP008210_028	2800001	291000
AP008210_029	2900001	301000
AP008210_030	3000001	311000
AP008210_031	3100001	321000
AP008210_032	3200001	331000
AP008210_033	3300001	341000
AP008210_034	3400001	351000
AP008210_035	3500001	361000
AP008210_036	3600001	371000
AP008210_037	3700001	381000
AP008210_038	3800001	391000
AP008210_039	3900001	401000
AP008210_040	4000001	411000
AP008210_041	4100001	421000
AP008210_042	4200001	431000
AP008210_043	4300001	441000
AP008210_044	4400001	451000
AP008210_045	4500001	461000
AP008210_046	4600001	471000
AP008210_047	4700001	481000
AP008210_048	4800001	491000
AP008210_049	4900001	501000
AP008210_050	5000001	511000
AP008210_051	5100001	521000
AP008210_052	5200001	531000
AP008210_053	5300001	541000
AP008210_054	5400001	551000
AP008210_055	5500001	561000
AP008210_056	5600001	571000
AP008210_057	5700001	581000
AP008210_058	5800001	591000
AP008210_059	5900001	601000
AP008210_060	6000001	611000
AP008210_061	6100001	621000
AP008210_062	6200001	631000
AP008210_063	6300001	641000

AP008210_064 6400001 6510000
AP008210_065 6500001 6610000
AP008210_066 6600001 6710000
AP008210_067 6700001 6810000
AP008210_068 6800001 6910000
AP008210_069 6900001 7010000
AP008210_070 7000001 7110000
AP008210_071 7100001 7210000
AP008210_072 7200001 7310000
AP008210_073 7300001 7410000
AP008210_074 7400001 7510000
AP008210_075 7500001 7610000
AP008210_076 7600001 7710000
AP008210_077 7700001 7810000
AP008210_078 7800001 7910000
AP008210_079 7900001 8010000
AP008210_080 8000001 8110000
AP008210_081 8100001 8210000
AP008210_082 8200001 8310000
AP008210_083 8300001 8410000
AP008210_084 8400001 8510000
AP008210_085 8500001 8610000
AP008210_086 8600001 8710000
AP008210_087 8700001 8810000
AP008210_088 8800001 8910000
AP008210_089 8900001 9010000
AP008210_090 9000001 9110000
AP008210_091 9100001 9210000
AP008210_092 9200001 9310000
AP008210_093 9300001 9410000
AP008210_094 9400001 9510000
AP008210_095 9500001 9610000
AP008210_096 9600001 9710000
AP008210_097 9700001 9810000
AP008210_098 9800001 9910000
AP008210_099 9900001 10010000
AP008210_100 10000001 10110000
AP008210_101 10100001 10210000
AP008210_102 10200001 10310000
AP008210_103 10300001 10410000
AP008210_104 10400001 10510000
AP008210_105 10500001 10610000
AP008210_106 10600001 10710000
AP008210_107 10700001 10810000
AP008210_108 10800001 10910000
AP008210_109 10900001 11010000
AP008210_110 11000001 11110000
AP008210_111 11100001 11210000
AP008210_112 11200001 11310000
AP008210_113 11300001 11410000
AP008210_114 11400001 11510000
AP008210_115 11500001 11610000
AP008210_116 11600001 11710000
AP008210_117 11700001 11810000
AP008210_118 11800001 11910000
AP008210_119 11900001 12010000
AP008210_120 12000001 12110000
AP008210_121 12100001 12210000
AP008210_122 12200001 12310000
AP008210_123 12300001 12410000
AP008210_124 12400001 12510000
AP008210_125 12500001 12610000
AP008210_126 12600001 12710000
AP008210_127 12700001 12810000
AP008210_128 12800001 12910000
AP008210_129 12900001 13010000
AP008210_130 13000001 13110000
AP008210_131 13100001 13210000
AP008210_132 13200001 13310000
AP008210_133 13300001 13410000
AP008210_134 13400001 13510000
AP008210_135 13500001 13610000
AP008210_136 13600001 13710000

AP008210_137 13700001 13810000
AP008210_138 13800001 13910000
AP008210_139 13900001 14010000
AP008210_140 14000001 14110000
AP008210_141 14100001 14210000
AP008210_142 14200001 14310000
AP008210_143 14300001 14410000
AP008210_144 14400001 14510000
AP008210_145 14500001 14610000
AP008210_146 14600001 14710000
AP008210_147 14700001 14810000
AP008210_148 14800001 14910000
AP008210_149 14900001 15010000
AP008210_150 15000001 15110000
AP008210_151 15100001 15210000
AP008210_152 15200001 15310000
AP008210_153 15300001 15410000
AP008210_154 15400001 15510000
AP008210_155 15500001 15610000
AP008210_156 15600001 15710000
AP008210_157 15700001 15810000
AP008210_158 15800001 15910000
AP008210_159 15900001 16010000
AP008210_160 16000001 16110000
AP008210_161 16100001 16210000
AP008210_162 16200001 16310000
AP008210_163 16300001 16410000
AP008210_164 16400001 16510000
AP008210_165 16500001 16610000
AP008210_166 16600001 16710000
AP008210_167 16700001 16810000
AP008210_168 16800001 16910000
AP008210_169 16900001 17010000
AP008210_170 17000001 17110000
AP008210_171 17100001 17210000
AP008210_172 17200001 17310000
AP008210_173 17300001 17410000
AP008210_174 17400001 17510000
AP008210_175 17500001 17610000
AP008210_176 17600001 17710000
AP008210_177 17700001 17810000
AP008210_178 17800001 17910000
AP008210_179 17900001 18010000
AP008210_180 18000001 18110000
AP008210_181 18100001 18210000
AP008210_182 18200001 18310000
AP008210_183 18300001 18410000
AP008210_184 18400001 18510000
AP008210_185 18500001 18610000
AP008210_186 18600001 18710000
AP008210_187 18700001 18810000
AP008210_188 18800001 18910000
AP008210_189 18900001 19010000
AP008210_190 19000001 19110000
AP008210_191 19100001 19210000
AP008210_192 19200001 19310000
AP008210_193 19300001 19410000
AP008210_194 19400001 19510000
AP008210_195 19500001 19610000
AP008210_196 19600001 19710000

Query Match 65.9%; Score 24.4; DB 4; Length 110000;
Best Local Similarity 82.4%; Pred. No. 7;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 4 TCGAATTCGGCTGAAAAAGCGTTGACC 37
Db 11954 TCGAATTCAGACTTGAAGAAAGCTTGTTGACC 11921

Search completed: May 19, 2006, 01:27:33
Job time : 794.333 secs

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CC catalytic domain and a catalytic domain from an accessory enzyme that is
 CC involved in formation of a nucleotide sugar which is a saccharide donor
 CC for a glycosyltransferase reaction. The fusion protein is useful in the
 CC enzymatic synthesis of oligosaccharides. The fusion proteins are able to
 CC catalyze more than one reaction involved in the enzymatic synthesis. This
 CC is useful for the development of therapeutic agents that have specific
 CC carbohydrate structures. Carbohydrates are involved in recognition
 CC elements on the surface of cells. The fusion protein can be used for the
 CC synthesis of both natural carbohydrates and synthetic derivatives with
 CC novel properties. The fusion polypeptide allows two glycosyltransferase
 CC reactions in a single vessel, provides improved yields of end products.
 CC Additionally, cleanup and disposal of extra solvents and by-products is
 CC reduced. The fusion protein can also use directly different donor
 CC analogues and various acceptors with a terminal galactose residue

Seq Sequence 37 BP, 9 A, 6 C, 11 G, 11 T, 0 U, 0 Other;
 Query Match 100.0%; Score 37; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

AAA81515/c
 ID AAA81515 standard; DNA; 16878 BP.

AC AAA81515;
 DT 04-DEC-2000 (first entry)
 DE N. meningitidis partial DNA sequence gum_62 SEQ ID NO:62.

XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; MenB; ds.

OS Neisseria meningitidis.

PN MO200022430-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99MO-US023573.

PR 09-OCT-1998; 98US-0103794P.

PR 30-APR-1999; 99US-0132068P.

PA (CHIR) CHIRON CORP.

PI Frazer CM, Hickey E, Peterson J, Tetelijn H, Venner JC,
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 PI Rappoli R, Pizzo M;

DR WPI; 2000-318079/27.

PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.

PS Claim 7; Page 1385-1390, 1760pp; English.

CC The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences,
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all

CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B, against all serotypes, and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC antigens have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions

Seq Sequence 16878 BP; 4598 A; 4598 C; 3853 G; 3827 T; 0 U; 2 Other;
 Query Match 71.4%; Score 26.4; DB 3; Length 16878;
 Best Local Similarity 96.4%; Pred. No. 1.3;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 3

AAA81490_09

Continuation (10 of 15) of AAA81490 from base 900001 (N. meningitidis B full length genom
 WP Sequence split into 15 fragments LOCUS AAA81490 Accession AAA81490

WP	Fragment Name	Begin	End
WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000
WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668

Query Match 71.4%; Score 26.4; DB 3; Length 110000;
 Best Local Similarity 96.4%; Pred. No. 1.8;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGGCTTGAAGGCTTGTGGAC 37
 Db 34748 TATGGGCTTGAAGGCTTGTGGAC 34775

RESULT 4
 ID AAF21609
 ID AAF21609 standard; DNA; 349980 BP.

AC AAF21609;

DT 13-MAR-2001 (first entry)

DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.

XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KW ds.

```
OS Neisseria meningitidis.
XX
XX MO200066791-A1.
XX
XX
XX 09-NOV-2000.
XX
XX 08-MAR-2000; 2000MO-US005928.
XX
XX 30-APR-1999; 99US-0132068P.
XX 08-OCT-1999; 99MO-US023573.
XX 28-FEB-2000; 2000GB-00004695.
XX
XX (CHIR ) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX
XX Pizza M, Hickey E, Peterson J, Tettein H, Venter JC,
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarsella M, Scarlato V;
PI Rappoli R, Frazer CM, Grandi G;
XX
XX MPI; 2000-647603/62.
XX
XX Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect, treat and prevent Neisserial infections.
XX
XX Claim 7; Appendix A; 692pp; English.
XX
XX The present invention describes the full length genome of Neisseria
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
CC long to go in a record on its own it was split into 8 sequences which
CC overlap each other at the beginning and end of each sequence by 49980 bp
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC primers which are used in the exemplification of the present invention.
CC The NMB genome and fragments from it have antibacterial activity, and can
CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC and/or antibodies which binds to the proteins can be used in compositions
CC for treating or preventing infection due to Neisserial bacteria or as a
CC diagnostic reagent for detecting the presence of Neisserial bacteria or
CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
CC computer storage medium or computer databases can be used in a search to
CC identify open reading frames (ORFs) or coding sequences within the NMB
CC genome. The DNA sequences provide further opportunities to find antigenic
CC or immunogenic proteins which are more effective in vaccines than the
CC outer membrane proteins currently used
XX
XX Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 U; 0 Other;
SQ
Query Match 71.4%; Score 26.4; DB 3; Length 349980;
Best Local Similarity 96.4%; Pred. No. 2.3;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 10 TCTGGCTTGAAGCTTGTGACC 37
Db 34749 TATGGCTTGAAGCTTGTGACC 34776
RESULT 5
AAFP21608
ID AAFP21608 standard; DNA; 349980 BP.
XX
XX AAFP21608;
XX
XX 13-MAR-2001 (first entry)
XX
XX Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX da.
XX
```

```
OS Neisseria meningitidis.
XX
XX MO200066791-A1.
XX
XX
XX 09-NOV-2000.
XX
XX 08-MAR-2000; 2000MO-US005928.
XX
XX 30-APR-1999; 99US-0132068P.
XX 08-OCT-1999; 99MO-US023573.
XX 28-FEB-2000; 2000GB-00004695.
XX
XX (CHIR ) CHIRON CORP.
XX (GENO-) INST GENOMIC RES.
XX
XX Pizza M, Hickey E, Peterson J, Tettein H, Venter JC,
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarsella M, Scarlato V;
PI Rappoli R, Frazer CM, Grandi G;
XX
XX MPI; 2000-647603/62.
XX
XX Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect, treat and prevent Neisserial infections.
XX
XX Claim 7; Appendix A; 692pp; English.
XX
XX The present invention describes the full length genome of Neisseria
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
CC long to go in a record on its own it was split into 8 sequences which
CC overlap each other at the beginning and end of each sequence by 49980 bp
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC primers which are used in the exemplification of the present invention.
CC The NMB genome and fragments from it have antibacterial activity, and can
CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC and/or antibodies which binds to the proteins can be used in compositions
CC for treating or preventing infection due to Neisserial bacteria or as a
CC diagnostic reagent for detecting the presence of Neisserial bacteria or
CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
CC computer storage medium or computer databases can be used in a search to
CC identify open reading frames (ORFs) or coding sequences within the NMB
CC genome. The DNA sequences provide further opportunities to find antigenic
CC or immunogenic proteins which are more effective in vaccines than the
CC outer membrane proteins currently used
XX
XX Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;
SQ
Query Match 71.4%; Score 26.4; DB 3; Length 349980;
Best Local Similarity 96.4%; Pred. No. 2.3;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 10 TCTGGCTTGAAGCTTGTGACC 37
Db 334749 TATGGCTTGAAGCTTGTGACC 334776
RESULT 6
AAV04125
ID AAV04125 standard; DNA; 1116 BP.
XX
XX AAV04125;
XX
XX 17-JUN-1998 (first entry)
XX
XX N. meningitidis alpha-2,3-sialyltransferase DNA.
XX
XX Alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid;
KW biologically active oligosaccharide; sialyl-modified protein; ss.
XX
XX Neisseria meningitidis.
OS
```

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XX Key Location/Qualifiers
FH CDS 1..116
FT /*tag= a
FT /product= "alpha-2,3-sialyl transferase"
PN MO9747749-A1.
XX
XX PD 18-DEC-1997.
XX PF 10-JUN-1997; 97WO-CA000390.
XX PR 10-JUN-1996; 96US-0019520P.
XX PR 07-JUN-1997; 97US-00872485.
XX
XX PA (CANA ) NAT RES COUNCIL CANADA.
XX
XX PI Gilbert M, Makarchuk WM, Young NM, Jennings MP,
XX DR WPI, 1998-05213/05.
XX DR P-PSDB; AAM41513.
XX
XX PT Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase -
XX PT useful to add sialic acid to acceptor with terminal galactose residue for
XX PT synthesis of biologically active oligosaccharide.
XX
XX PS Claim 4; Page 37-38; 50pp; English.
XX
XX CC This sequence encodes an alpha-2,3-sialyltransferase which has been
XX CC isolated from Neisseria meningitidis. The protein can be used as a
XX CC reagent for adding a sialic acid residue to an acceptor having a terminal
XX CC galactose residue, e.g. in synthesis of biologically active
XX CC oligosaccharides or sialyl-modified proteins or lipids. The nucleic acid
XX CC sequence can be used for the recombinant production of alpha-2,3-
XX CC sialyltransferase
XX
XX SQ Sequence 1116 BP; 306 A; 231 C; 292 G; 287 T; 0 U; 0 Other;
XX
XX Query Match 70.3%; Score 26; DB 2; Length 1116;
XX Best Local Similarity 100.0%; Pred. No. 1.1;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 TGGGCTTGAAAAAGCGCTGTGTGACC 37
XX Db 2 TGGGCTTGAAAAAGCGCTGTGTGACC 27
XX
XX RESULT 7
XX AAH07120
XX ID AAH07120 standard; cDNA; 726 BP.
XX AC AAH07120;
XX
XX DT 26-JUN-2001 (first entry)
XX
XX DE Human cDNA clone (5'-primer) SEQ ID NO:3955.
XX
XX KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1074617-A2.
XX
XX PD 07-FEB-2001.
XX
XX PF 28-JUL-2000; 2000EP-00116126.
XX
XX PR 29-JUL-1999; 99JP-00248036.
XX PR 27-AUG-1999; 99JP-00300253.
XX PR 11-JAN-2000; 2000JP-00118776.
XX PR 02-MAY-2000; 2000JP-00183767.
XX PR 09-JUN-2000; 2000JP-00241899.
XX

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PA (HELI-) HELIX RES INST.
XX
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX DR WPI; 2001-318749/34.
XX
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX PT length cDNAs defined in the specification, and for the detection and/or
XX PT diagnosis of the abnormality of the proteins encoded by the full-length
XX PT cDNAs.
XX
XX PS Claim 1; SEQ ID NO 3955; 2537p + Sequence listing; English.
XX
XX CC The present invention describes primer sets for synthesizing 5602 full-
XX CC length cDNAs defined in the specification, where a primer set comprises:
XX CC (a) an oligo-dT primer and an oligonucleotide complementary to the
XX CC complementary strand of a polynucleotide which comprises one of the 5602
XX CC nucleotide sequences defined in the specification, where the
XX CC or an oligonucleotide comprising a sequence complementary to the
XX CC complementary strand of a polynucleotide which comprises a 5'-end
XX CC sequence and an oligonucleotide comprising a sequence complementary to a
XX CC polynucleotide which comprises a 3'-end sequence, where the
XX CC the 5'-end sequence comprises at least 15 nucleotides, and the combination of
XX CC the gene therapy. The primer sets can be used in antisense therapy and in
XX CC particularly full-length cDNAs. The primers are also useful for the
XX CC detection and/or diagnosis of the abnormality of the proteins encoded by
XX CC the full-length cDNAs. The primers allow obtaining of the full-length
XX CC cDNAs easily without any specialized methods. AAH31636 to AAH31628 and
XX CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
XX CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX CC present invention
XX
XX SQ Sequence 726 BP; 193 A; 171 C; 171 G; 188 T; 0 U; 3 Other;
XX
XX Query Match 63.8%; Score 23.6; DB 4; Length 726;
XX Best Local Similarity 83.9%; Pred. No. 10;
XX Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 5 GGAATTCTGGGCTTGAAAAAGCGCTGTGTA 35
XX Db 633 GNACTTCGGGCTTGAAAAAGACTTGCTTGA 663
XX
XX RESULT 8
XX ABL19064/C
XX ID ABL19064 standard; DNA; 2613 BP.
XX AC ABL19064;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8665.
XX
XX KM Drosophila; developmental biology; cell signalling; insecticide;
XX KM pharmaceutical; gene; ds.
XX
XX OS Drosophila melanogaster.
XX
XX PN WO200171042-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX
XX PA (PEKE ) PE CORP NY.

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XX Venter JC, Adams M, Li FMD, Myers EM;
PI WPI; 2001-656860/75.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PI interactions.
XX
PS Claim 1; SEQ ID NO 8665; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins (AB57737-
CC AB572072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2613 BP; 796 A; 530 C; 543 G; 744 T; 0 U; 0 Other;
XX
Query Match 62.7%; Score 23.2; DB 4; Length 2613;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
Qy 1 GCATGCAATTCGGCTTGAAGGCTGTTGAC 36
Db 2436 GAATCGATTCTAGGCTTTCAAGGCTGTTTAC 2401
XX
RESULT 9
AB211361
ID AB211361 standard; cDNA; 1734 BP.
XX
AC AB211361;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polynucleotide SEQ ID NO 243.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antithrptic; gene; ss.
XX
XX Homo sapiens.
XX
OS WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F,
PI Xue AY, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
XX
DR P-PSDB; ABP69144.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,

PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 1; SEQ ID NO 243; 1012pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (AB211119-
CC AB212066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1734 BP; 523 A; 385 C; 392 G; 434 T; 0 U; 0 Other;
XX
Query Match 62.2%; Score 23; DB 6; Length 1734;
Best Local Similarity 83.9%; Pred. No. 22;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
Qy 5 GCAATTCGGCTTGAAGGCTGTTGCA 35
Db 589 GAATCTTGCGCTTAAAGACTTCTTCA 619
XX
RESULT 10
ADM43879
ID ADM43879 standard; cDNA; 1734 BP.
XX
AC ADM43879;
XX
DT 03-JUN-2004 (first entry)
XX
DE Novel human arginine-rich protein cDNA #243.
XX
KW ss; gene; human; arginine-rich protein; cancer; inflammation;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN US2004053250-A1.
XX
PD 18-MAR-2004.
XX
PF 21-NOV-2002; 2002US-00302172.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PR 05-MAR-2002; 2002WO-US005095.
XX
PR 20-AUG-2002; 2002US-00225251.
XX
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
XX
PI Tang YT, Xue A, Drmanac RT;
XX
DR WPI; 2004-238579/22.
XX
XX New isolated arginine-rich protein-like polynucleotides and polypeptides,
PT useful for diagnosing and/or treating conditions associated with aberrant
PT activity of the arginine-rich polypeptides, such as cancer and
PT inflammation.
XX
XX Disclosure; SEQ ID NO 243; 51pp; English.
XX

CC The invention relates to an isolated polynucleotide. The methods and
 CC compositions of the present invention are useful for the diagnosis and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the arginine-rich protein-like polypeptides, such as
 CC cancer and inflammation. They can also be used in forensics, gene
 CC mapping, identification of mutations responsible for genetic disorders,
 CC and in assessing biodiversity. The present sequence represents a novel
 CC human arginine-rich protein cDNA.

SO Sequence 1734 BP; 523 A; 385 C; 392 G; 434 T; 0 U; 0 Other;

Query Match 62.2%; Score 23; DB 12; Length 1734;
 Best Local Similarity 83.9%; Pred. No. 22;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTTGTGA 35
 Db 589 GAACCTTCGGGCTTGAAGAGCTTGTGA 619

RESULT 11

AAH16361
 ID AAH16361 standard; cDNA; 2228 BP.

AC AAH16361;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:15295.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PM EPI074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-00116126.

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Iehi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.

PS Claim 8; SEQ ID NO 15295; 2537bp + Sequence Listing; English.

CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises at least 15 nucleotides, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination
 CC of the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in

CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH16742 represent human cDNA sequences; AAH92446 to AAH95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention

SO Sequence 2228 BP; 662 A; 462 C; 474 G; 630 T; 0 U; 0 Other;

Query Match 62.2%; Score 23; DB 4; Length 2228;
 Best Local Similarity 83.9%; Pred. No. 23;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTTGTGA 35
 Db 633 GAACCTTCGGGCTTGAAGAGCTTGTGA 663

RESULT 12

ADQ84099
 ID ADQ84099 standard; cDNA; 2228 BP.

AC ADQ84099;

DT 07-OCT-2004 (first entry)

DE Human tumour-associated antigenic target (TAT) cDNA sequence #913.

human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;
 cancer; cell proliferative disorder; gene; ss.

OS Homo sapiens.

PN WO2004060270-A2.

PD 22-JUL-2004.

PF 15-OCT-2003; 2003WO-US029126.

PR 18-OCT-2002; 2002US-041988P.

PA (GETH) GENENTECH INC.

PI (WUTD/) WU T D.

PI (ZHOU/) ZHOU Y.

PI Wu TD, Zhou Y;

DR WPI; 2004-534300/51.

PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.

PS Claim 1; SEQ ID NO 913; 5504bp; English.

CC The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 CC sequence identity to (a) or (b); (e) a sequence that hybridizes to (a) -
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC comprising the above polypeptide fused to a heterologous polypeptide;
 CC for producing the antibody that binds to the above polypeptide; (7) a process
 CC for producing the antibody; (8) an isolated oligopeptide that binds to
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)

CC binding organic molecule that binds to the above polypeptide; (10) a
 CC composition of matter comprising the above (chimeric) polypeptide;
 CC antibody, oligopeptide or TAT binding organic molecule, in combination
 CC with a carrier; (11) an article of manufacture comprising a container and
 CC the composition of matter contained within the container; (12) methods of
 CC inhibiting the growth of a cell that expresses the above protein, where
 CC the growth of the cell is at least in part dependent upon a growth
 CC potentiating effect of the above protein; (13) a method of
 CC therapeutically treating a mammal having a cancerous tumour comprising
 CC cells that express the above protein; (14) a method of determining the
 CC presence of a protein in a sample suspected of containing the protein
 CC described above; (15) methods of diagnosing the presence of a tumour in a
 CC mammal; (16) a method for treating or preventing a cell proliferative
 CC disorder associated with increased expression or activity of the above
 CC protein; and (17) a method of binding an antibody, oligopeptide or
 CC organic molecule to a cell that expresses the protein described above.
 CC The TAT sequences have cytostatic activities, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing,
 CC preventing or treating cancer. The composition is also used for preparing
 CC a medicament for the therapeutic treatment or diagnostic detection of a
 CC cell proliferative disorder or cancer. The present sequence represents a
 CC human TAT cDNA sequence from the present invention.

XX
 SQ Sequence 2228 BP; 663 A; 460 C; 475 G; 630 T; 0 U; 0 Other;
 Query Match 62.2%; Score 23; DB 12; Length 2228;
 Best Local Similarity 83.9%; Pred. No. 23;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATCTGGGCTGAAAAGGCTTGTGA 35
 |||||
 Db 633 GAACCTCTGGGCTTTAAAAGACTTCTTGA 663

RESULT 13
 AAL61230
 ID AAL61230 standard; cDNA; 2942 BP.
 AC AAL61230;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE Human secreted protein (SECP)-1 cDNA.
 XX
 KW Human; secreted protein; SECP; neurodegenerative disorder; scleroderma;
 KW Parkinson's disease; Alzheimer's disease; myotonic dystrophy; leukaemia;
 KW muscular disorder; systemic lupus erythematosus; renal disorder; cancer;
 KW immunological disorder; gastrointestinal disorder; catatonias; infection;
 KW diabetes; Goodpasture's syndrome; cardiovascular disorder; gene therapy;
 KW endocrine disorder; atherosclerosis; transgenic animal; Grave's disease;
 KW allergy; Crohn's disease; hepatic disease; cirrhosis; transgenic; gene;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT CDS 232..2133
 FT /tag= a
 FT /product= "Human SECP protein"
 XX
 PN WO2003046196-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 21-NOV-2002; 2002WO-US037803.
 XX
 PR 28-NOV-2001; 2001US-0334229P.
 PR 07-DEC-2001; 2001US-0339236P.
 PR 21-DEC-2001; 2001US-0343555P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Baughn MR, Becha SD, Chawla NK, Emerling BM, Fu G, Ison CH;

PI jin P, Kabie AE, Lal PG, Lee S, Marguis JP, Lehr-Mason PM;
 PI Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Wang JT, Warren BA;
 PI Yue H, Zebbarjadian Y, Das D;
 XX
 DR WPI; 2003-505207/47.
 DR P-PSDB; AAO30398.
 XX
 PT New SECP polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with an abnormal expression or activity of SECP,
 PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer
 PT and/or infections.
 XX
 PS Claim 5; Page 170-171; 194pp; English.

XX
 CC The invention relates to human secreted proteins (SECP) and nucleic acid
 CC molecules encoding such proteins. SECP sequences are useful in
 CC diagnosing, preventing and treating disorders associated with an abnormal
 CC expression or activity of SECP such as neurodegenerative disorders (e.g.
 CC Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.
 CC myotonic dystrophy, catatonias), endocrine disorders (e.g. diabetes,
 CC Grave's disease), cancers (e.g. leukaemia, cervical or breast cancers),
 CC immunological disorders (e.g. scleroderma, systemic lupus erythematosus,
 CC allergies), gastrointestinal disorders (e.g. Crohn's disease), renal
 CC disorders (e.g. Goodpasture's syndrome), infections (e.g. viral, fungal,
 CC bacterial, parasitic, protozoal, helminthic), cardiovascular disorders
 CC (e.g. atherosclerosis) or hepatic diseases (e.g. cirrhosis). SECP
 CC polynucleotides can be used to create humanised animals or transgenic
 CC animals to model human disease. The invention is useful in gene therapy.
 CC The present sequence is human SECP protein encoding cDNA
 XX

SQ Sequence 2942 BP; 883 A; 624 C; 656 G; 779 T; 0 U; 0 Other;
 Query Match 62.2%; Score 23; DB 9; Length 2942;
 Best Local Similarity 83.9%; Pred. No. 24;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATCTGGGCTGAAAAGGCTTGTGA 35
 |||||
 Db 613 GAACCTCTGGGCTTTAAAAGACTTCTTGA 643

RESULT 14
 AAX10673/c
 ID AAX10673 standard; DNA; 225 BP.
 XX
 AC AAX10673;
 XX
 DT 30-MAR-1999 (first entry)
 XX
 DE Human biallelic polymorphic DNA fragment WI-6315.
 XX
 KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
 KW treatment; marker; ss.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT CDS WO9820165-A2.
 FT /tag= a
 FT /product= "Human SECP protein"
 XX
 PN WO9820165-A2.
 XX
 PD 14-MAY-1998.
 XX
 PF 05-NOV-1997; 97WO-US020313.
 XX
 PR 06-NOV-1996; 96US-0030455P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Lander ES, Wang D, Hudson T;
 XX
 DR WPI; 1998-286974/25.
 XX
 PT New isolated nucleic acid segments from the human genome - used for

PT determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease.

Claim 1; Page 70; 310pp; English.

CC AAX10269-X12937 are human DNA fragments which contain biallelic
 CC polymorphic markers which have been isolated using the primers
 CC represented in AAX09121-X10268. The base occupying the polymorphic site
 CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
 CC can be used in methods for determining polymorphic forms in an individual
 CC for use in e.g. forensics, paternity testing or for phenotypic typing for
 CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
 CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
 CC familial hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases

SQ Sequence 225 BP; 55 A; 51 C; 46 G; 72 T; 0 U; 1 Other;

Query Match 61.6%; Score 22.8; DB 2; Length 225;
 Best Local Similarity 79.4%; Pred. No. 18;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 GCATGGAATTCTGGGCTTGAAGGCTGTTTG 34
 DB 100 GCATGACACGCTGGCTTGAAGGACCTGTTTG 67

RESULT 15

AAX10672/c
 ID AAX10672 standard; DNA; 225 BP.

XX AAX10672;

DT 30-MAR-1999 (first entry)

DE Human biallelic polymorphic DNA fragment WI-6315b.

KM Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KM detection; phenotypic typing; characteristic; infection; hereditary;
 KM autoimmune disease; cancer; inflammation; drug; therapy; medication;
 KM treatment; marker; ss.

OS Homo sapiens.

PN WO9820165-A2.

PD 14-MAY-1998.

PF 05-NOV-1997; 97WO-US020313.

PR 06-NOV-1996; 96US-0030455P.

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

PI Lander ES, Wang D, Hudson T;

DR WPI; 1998-286974/25.

PT New isolated nucleic acid segments from the human genome - used for
 PT determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease.

PS Claim 1; Page 70; 310pp; English.

CC AAX10269-X12937 are human DNA fragments which contain biallelic
 CC polymorphic markers which have been isolated using the primers
 CC represented in AAX09121-X10268. The base occupying the polymorphic site
 CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
 CC can be used in methods for determining polymorphic forms in an individual
 CC for use in e.g. forensics, paternity testing or for phenotypic typing for
 CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
 CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
 CC familial hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases

SQ Sequence 225 BP; 55 A; 50 C; 46 G; 73 T; 0 U; 1 Other;

Query Match 61.6%; Score 22.8; DB 2; Length 225;
 Best Local Similarity 79.4%; Pred. No. 18;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 GCATGGAATTCTGGGCTTGAAGGCTGTTTG 34
 DB 100 GCATGACACGCTGGCTTGAAGGACCTGTTTG 67

Search completed: May 19, 2006, 00:53:17
 Job time : 180.906 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 00:53:30 ; Search time 1485.78 Seconds

(without alignments)
1392.544 Million cell updates/sec

Title: US-09-211-691-5

Perfect score: 37

Sequence: 1 gcatggaatccggtctgaaagagctgttacc 37

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25.8	69.7	901	4	AI325176
2	25.4	68.6	618	4	C80292
3	24.4	65.9	1443	13	CL969122
4	24.4	65.9	1446	13	CL970741
5	24	64.9	663	7	BB642392
C 6	23.8	64.3	635	5	CF295692
7	23.8	64.3	828	14	CR109858
8	23.8	64.3	843	14	CR207976
9	23.8	64.3	884	14	CR26869
10	23.8	64.3	912	14	CR050996
11	23.6	63.8	726	1	AU133964
12	23.4	63.2	725	11	AZ192473
13	23.2	62.7	663	2	BI096984
14	23	62.2	453	2	BF744479
15	23	62.2	498	12	CG614466
16	23	62.2	507	9	DB047668
17	23	62.2	518	9	DB021107
18	23	62.2	527	12	CG596353
19	23	62.2	530	9	DB056413

20	23	62.2	563	9	DB049403	DB049403
21	23	62.2	565	9	DB051314	DB051314
22	23	62.2	566	9	DB031260	DB031260
23	23	62.2	567	7	AW962292	AW962292
24	23	62.2	574	9	DB039479	DB039479
25	23	62.2	598	9	DB031132	DB031132
26	23	62.2	600	8	CV024531	CV024531
27	23	62.2	674	7	BB617250	BB617250
28	23	62.2	685	2	BG773112	BG773112
29	23	62.2	709	4	BY171855	BY171855
30	23	62.2	815	5	CJ488602	BB615455
31	23	62.2	818	5	CJ488602	BB615455
32	23	62.2	822	14	CR040392	CJ488602
C 33	23	62.2	832	5	CD632278	BG771738
34	23	62.2	832	5	CD632278	BG771738
35	23	62.2	1891	14	AY404519	CG604392
36	23	62.2	1911	14	AY404517	Forward s
37	23	62.2	1911	14	AY404518	CD632278
38	23	62.2	1928	6	AK037169	AY404519
39	23	62.2	1976	6	AK044441	AY404517
40	23	62.2	2224	6	AK020021	AY404518
41	23	62.2	2393	6	AK029724	AK037169
42	23	62.2	3455	6	AK033409	AK044441
C 43	22.8	61.6	226	10	Z38338	AK020021
C 44	22.8	61.6	366	10	T15936	AK029724
C 45	22.8	61.6	464	4	BX103153	AK033409

ALIGNMENTS

RESULT 1
AI325176/c 901 bp mRNA linear EST 23-DEC-1998
LOCUS mes01h12.x1 Stratagene mouse embryonic carcinoma (#937317) Mus
DEFINITION musculus cDNA clone IMAGE:605735 3' similar to gb:D16141 Mouse
mg1-1 mRNA for ORF, complete cds (MOUSE);, mRNA sequence.

ACCESSION AI325176
VERSION AI325176.1 GI:4059605
KEYWORDS
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

REFERENCE

1 (bases 1 to 901)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HM Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HM Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through INLTL; contact the
IMAGE Consortium (info@image.lnlnl.gov) for further information.
MG1:371167
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 432.
Location/Qualifiers
1. 901
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:605735"
/issue_type="carcinoma"

TITLE

JOURNAL
COMMENT
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HM Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through INLTL; contact the
IMAGE Consortium (info@image.lnlnl.gov) for further information.
MG1:371167
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 432.
Location/Qualifiers
1. 901
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:605735"
/issue_type="carcinoma"

/dev stage="embryonic"
 /lab host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse embryonic carcinoma
 (#93717)"
 /note="Vector: plusescript SK-; Site 1: EcoRI, site 2:
 XhoI; Cloned unidirectionally. Primer: Oligo dt. p19 cell
 line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
 adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

ORIGIN

Query Match 69.7%; Score 25.8; DB 1; Length 901;
 Best Local Similarity 81.1%; Pred. No. 17;
 Matches 30; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCATGAAATTCCTGGCTTGAAGGCTTGTGACC 37
 Db 823 GCATGAAATTCCTGGCTTGAAGGCTTGTGACC 787

RESULT 2

LOCUS C80292 618 bp mRNA linear EST 26-JUN-1998
 DEFINITION J0079C07 3' similar to Human mRNA for KIAA0312 gene, mRNA sequence.
 ACCESSION C80292
 VERSION C80292.1 GI:2520622
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Euteleostomi; Euteleostomi; Euteleostomi; Euteleostomi;
 Sciurognathia; Muridae; Muridae; Muridae; Muridae; Muridae;
 1 (bases 1 to 618)
 Ko, M.S.H., Kitchen, J.R., Wang, X., Wang, X., Threat, T.A., Sun, T.,
 Grabovac, M.J., Mason, S., Lim, M.K., Paonessa, P.D., Sauls, A.D. and
 Doi, H.

TITLE Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst
 (The ERATO/Doi Project at Wayne State University)
 JOURNAL Unpublished (1997)
 COMMENT Contact: Hirofumi Doi
 Doi Biosymmetry Project, ERATO
 Japan Science and Technology Corporation (JST)
 MBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
 Email: hdo@doi.jst.go.jp.
 Location/Qualifiers

FEATURES
 source
 1..618
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="J0079C07"
 /issue_type="blastocyst"
 /dev_stage="3.5-dpc"
 /clone_lib="Mouse 3.5-dpc blastocyst cDNA"

ORIGIN

Query Match 69.6%; Score 25.4; DB 4; Length 618;
 Best Local Similarity 82.9%; Pred. No. 22;
 Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 ATGGAATTCCTGGCTTGAAGGCTTGTGACC 37
 Db 576 ATGGAATTCCTGGCTTGAAGGCTTGTGACC 610

RESULT 3

LOCUS CL969122 1443 bp DNA linear GSS 21-SEP-2004
 DEFINITION OaIFCC017869 Oryza sativa Expressed Library Oryza sativa (indica
 cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL969122
 VERSION CL969122.1 GI:52392873

KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
 1 (bases 1 to 1443)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G.K.S., Deng, X.W. and Wang, J.

TITLE An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 JOURNAL Unpublished (2004)
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80486676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.

FEATURES

source
 1..1443
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39946"
 /clone_lib="Oryza sativa Expressed Library"
 /note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 65.9%; Score 24.4; DB 13; Length 1443;
 Best Local Similarity 82.4%; Pred. No. 70;
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 TGAATTCCTGGCTTGAAGGCTTGTGACC 37
 Db 532 TGAATTCCTGGCTTGAAGGCTTGTGACC 565

RESULT 4
 LOCUS CL970741 1446 bp DNA linear GSS 21-SEP-2004
 DEFINITION OaIFCC020412 Oryza sativa Expressed Library Oryza sativa (indica
 cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL970741
 VERSION CL970741.1 GI:52396091
 KEYWORDS GSS.

ORGANISM Oryza sativa (indica cultivar-group)
 Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
 1 (bases 1 to 1446)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G.K.S., Deng, X.W. and Wang, J.

TITLE An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 JOURNAL Unpublished (2004)
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomic
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80486676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.

FEATURES

source
 1..1446
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"

/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 65.9%; Score 24.4; DB 13; Length 1446;
Best Local Similarity 82.4%; Pred. No. 70;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 TGAATTCTGGGCTTGAAGGCTTTGACC 37
|||||
532 TGAATCAGAGCTTGAAGGCTTTGACC 565

RESULT 5
BB642392 663 bp mRNA linear EST 26-OCT-2001
LOCUS BB642392 RIKEN full-length enriched, adult retina Mus musculus cDNA
DEFINITION clone A930013F09 5', mRNA sequence.
BB642392
BB642392.1 GI:16477311
EST.
Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 663)
Hara,A., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Konda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
TITLE Contact: Yoshihide Hayashizaki
JOURNAL Laboratory for Genome Exploration Research Group, RIKEN Genomic
COMMENT Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Shohiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10): 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Oawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamashita,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
location/Qualifiers
1. .663
/organism="Mus musculus"

/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A930013F09"
/issue="retina"
/tissue_type="retina"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult retina"
/note="Site 1: Salt; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'GAGAGAGATCTCGACTTATTATTATTTATTTCCCTCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. -Retina RNA was provided by Stefano Guerinich, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA02115, USA, whose assistance we gratefully acknowledge."

ORIGIN

Query Match 64.9%; Score 24; DB 7; Length 663;
Best Local Similarity 84.4%; Pred. No. 86;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TGAATTCTGGGCTTGAAGGCTTTGACC 35
|||||
567 TGAATCTGGGCTTGAAGGCTTTGACC 598

RESULT 6
CF295692 635 bp mRNA linear EST 14-AUG-2003
LOCUS CF295692 30DGS--05-L22.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 30DGS--05-L22, mRNA
sequence.
CF295692
CF295692.1 GI:33664725
EST.
Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 635)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
location/Qualifiers
1. .635
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--05-L22"
/issue="leaf"
/dev_stage="30 days after germination"

/lab host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DS)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Query Match 64.3%; Score 23.8; DB 5; Length 635;
 Best Local Similarity 80.0%; Pred. No. 1e+02;
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 ATGGAATTCCTGGCTGAAAAAGCTTGTGGACC 37
 Db 211 ATGAAATTTTGGCTGAAAAACGCTTGTGGCC 177

RESULT 7
 CR109858
 LOCUS

DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
 chromosome engineering clone MHPN180g24, genomic survey sequence.
 CR109858
 VERSION CR109858.1 GI:49857273
 KEYWORDS GSS: genome survey sequence; MICR.
 SOURCE Mus musculus (house mouse)
 ORGANISM

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 828)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES
 source
 1..828
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN180g24"
 /clone_lib="MHPN"

ORIGIN

Query Match 64.3%; Score 23.8; DB 14; Length 828;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCATGGAATTCCTGGCTGAAAAAGCTTGTGGA 35
 Db 656 GCATGGAATTCCTGTTGAATATATCGTTGA 690

RESULT 8
 CR207976
 LOCUS

DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
 chromosome engineering clone MHPN184k16, genomic survey sequence.
 CR207976
 VERSION CR207976.1 GI:49986825
 KEYWORDS GSS: genome survey sequence; MICR.
 SOURCE Mus musculus (house mouse)
 ORGANISM

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 843)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. http://www.sanger.ac.uk/MICR
 Location/Qualifiers
 1..843
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN184k16"
 /clone_lib="MHPN"

ORIGIN

Query Match 64.3%; Score 23.8; DB 14; Length 843;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCATGGAATTCCTGGCTGAAAAAGCTTGTGGA 35
 Db 648 GCATGGAATTCCTGTTGAATATATCGTTGA 682

RESULT 9
 CR126869
 LOCUS

DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
 chromosome engineering clone MHPN78a07, genomic survey sequence.
 CR126869
 VERSION CR126869.1 GI:49874321
 KEYWORDS GSS: genome survey sequence; MICR.
 SOURCE Mus musculus (house mouse)
 ORGANISM

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 844)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES
 source
 1..844
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN78a07"
 /clone_lib="MHPN"

ORIGIN

Query Match 64.3%; Score 23.8; DB 14; Length 884;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCATGGAATTCCTGGCTGAAAAAGCTTGTGGA 35
 Db 656 GCATGGAATTCCTGTTGAATATATCGTTGA 690

RESULT 10
 CR050996
 LOCUS

DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
 chromosome engineering clone MHPN71g17, genomic survey sequence.
 CR050996
 VERSION CR050996.1 GI:49784135
 KEYWORDS GSS: genome survey sequence; MICR.
 SOURCE Mus musculus (house mouse)
 ORGANISM

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 912)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.

TITLE Rogers, J. and Bradley, A.
 JOURNAL Direct Submission
 FEATURES Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 source CB10 ISA, UK. http://www.sanger.ac.uk/MICER
 Location/Qualifiers
 1..912
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHEN71917"
 /clone_id="MHEN"
 ORIGIN
 Query Match 64.3%; Score 23.8; DB 14; Length 912;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 GCATGAATTCCTGGCTGAAAAGGCTTGTGA 35
 661 GCATGAATTCCTGGCTTGAATATATCTTTGA 695
 RESULT 11
 AUI33964 726 bp mRNA linear EST 01-AUG-2002
 LOCUS AUI33964 OVARC1 Homo sapiens cDNA clone OVARC1001010 5', mRNA
 DEFINITION sequence.
 ACCESSION AUI33964
 VERSION AUI33964.1 GI:10994503
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 1 (bases 1 to 726)
 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Tsutsumi, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Magatsuna, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FUJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdn@nifty.com
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
 1..726
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="OVARC1001010"
 /cissue_type="ovary, tumor tissue"
 /clone_id="OVARC1"
 /note="Vector: pME18SFL3"
 ORIGIN
 Query Match 63.8%; Score 23.6; DB 1; Length 726;
 Best Local Similarity 83.9%; Pred. No. 1.3e+02;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GAATTCGGGCTTGAAAAGGCTTGTGA 35
 DB 633 GNACTTCGGGCTTTAAAGAACTTGTGA 663
 RESULT 12
 A2192473 725 bp DNA linear GSS 30-AUG-2000
 LOCUS SP_1021.B1.E08.SPE8 Strongylocentrotus purpuratus, purple sea
 DEFINITION urchin, sperm genomic BAC library Strongylocentrotus purpuratus
 genomic clone Plate=1021 Col=15 Row=J, genomic survey sequence.
 A2192473
 A2192473 GI:8375752
 ACCESSION GSS.
 VERSION Strongylocentrotus purpuratus
 KEYWORDS Strongylocentrotus purpuratus
 SOURCE Strongylocentrotus purpuratus
 ORGANISM Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Echinoidea; Echinacea; Echinoidea;
 Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 725)
 Cameron, R.A., Mahatras, G., Rast, J.P., Martinez, P., Biondi, T.R.,
 Swartzell, S., Wallace, J.C., Pousetka, A.J., Livingston, B.T.,
 Wray, G.A., Eitensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H.
 and Hood, L.
 A sea urchin genome project: Sequence scan, virtual map, and
 additional resources
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 10920195
 Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 1021 row: J column: 15
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 725.
 Location/Qualifiers
 1..725
 /organism="Strongylocentrotus purpuratus"
 /mol_type="genomic DNA"
 /db_xref="taxon:7668"
 /clone="Plate=1021 Col=15 Row=J"
 /clone_id="Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli
 DH10B"
 ORIGIN
 Query Match 63.2%; Score 23.4; DB 11; Length 725;
 Best Local Similarity 81.8%; Pred. No. 1.6e+02;
 Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GCATGAATTCCTGGCTGAAAAGGCTTGT 33
 DB 360 GCATGCATTCCTGGCCAGAAAAGGCTGTAT 392
 RESULT 13
 B1096984 663 bp mRNA linear EST 25-JUN-2001
 LOCUS SCUM32-DB1-1 Melaleuca alternifolia (Cheel) mRNA Melaleuca
 DEFINITION alternifolia cDNA, mRNA sequence.
 ACCESSION B1096984
 VERSION B1096984.1 GI:14548641
 KEYWORDS EST.
 SOURCE Melaleuca alternifolia (tea tree)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Myrtales; Myrtaceae; Melaleuca.

REFERENCE 1 (bases 1 to 663)
 AUTHORS Shelton,D., Leach,D., Beverstock,P and Henry,R.
 TITLE Isolation of genes involved in secondary metabolism from *Melaleuca alternifolia* (Cheel) using expressed sequence tags (ESTs)
 JOURNAL Plant Sci. 162 (1), 9-15 (2002)
 COMMENT Contact: Shelton D
 Centre for Plant Conservation Genetics
 Southern Cross University
 P.O. Box 157, Lismore, NSW 2480, Australia
 Tel: 61 2 6620 3173
 Fax: 61 2 6622 2080
 Email: dshelton@scu.edu.au.
 Location/Qualifiers
 source 1..663
 /organism="Melaleuca alternifolia"
 /mol_type="mRNA"
 /db_xref="taxon:164405"
 /clone_lib="Melaleuca alternifolia (Cheel) mRNA"

ORIGIN
 Query Match 62.7%; Score 23.2; DB 2; Length 663;
 Best Local Similarity 75.7%; Pred. No. 1.9e+02;
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 GCATGAATTCCTGGGCTTGAAGAGCTTGTGACC 37
 345 GCTTGAATTCGAGACTTGAGAGGCTTGTGTTACC 381

Db
 1 GCATGAATTCCTGGGCTTGAAGAGCTTGTGACC 37
 345 GCTTGAATTCGAGACTTGAGAGGCTTGTGTTACC 381

RESULT 14
 B7744479 453 bp mRNA linear EST 10-JAN-2001
 LOCUS QV2-B70636-291000-443-a01 B70636 Homo sapiens cDNA, mRNA sequence.
 ACCESSION B7744479
 VERSION B7744479.1 GI:12071155
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 453)
 Dias Neco,E., Garcia Correa,R., Verjowski-Almeida,S., Britones,M.R.,
 Negat,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalhaes,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&ct=QV2-B70636-
 291000-443-a01&ct3=2000-10-29&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 453.
 Location/Qualifiers
 source 1..453
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="B70636"

/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 62.2%; Score 23; DB 2; Length 453;
 Best Local Similarity 83.9%; Pred. No. 2.1e+02;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTTGTGTA 35
 378 GAACCTTCGGGCTTGAAGAGCTTGTGTA 408

Db
 5 GGAATTCGGGCTTGAAGAGCTTGTGTA 35
 378 GAACCTTCGGGCTTGAAGAGCTTGTGTA 408

RESULT 15
 CG614466 498 bp mRNA linear GSS 02-OCT-2003
 LOCUS OSTR302754 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTR302754,
 mRNA sequence.
 ACCESSION CG614466
 VERSION CG614466.1 GI:37438315
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 498)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggott,J., Beltrando-Rio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Kipp,P., Kohlhautf.,B., Ma,Z.-Q., Mackesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,W.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Pearson,C. and Sands,A.T.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 14610273
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap

TITLE
 JOURNAL
 PUBMED
 COMMENT
 Location/Qualifiers
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 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OSTR302754"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
 Query Match 62.2%; Score 23; DB 12; Length 498;
 Best Local Similarity 83.9%; Pred. No. 2.1e+02;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 GGAATTCGGGCTTGAAGAGCTTGTGTA 35
 408 GAACCTTCGGGCTTGAAGAGCTTGTGTA 438

Db
 5 GGAATTCGGGCTTGAAGAGCTTGTGTA 35
 408 GAACCTTCGGGCTTGAAGAGCTTGTGTA 438

Search completed: May 19, 2006, 02:31:54
 Job time : 1489.78 secs

Fri May 19 11:37:23 2006

us-09-211-691-5.rst

Page 7

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 01:27:44 ; Search time 59.3542 Seconds

(Without alignments)
1166.405 Million cell updates/sec

Title: US-09-211-691-5

Perfect score: 37
Sequence: 1 gcatggaatcttggtgctgaaagctcttgacc 37Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /EMC_Celerra_SIDS3/prodata/2/ina/5/COMB.seq:*
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- 8: /EMC_Celerra_SIDS3/prodata/2/ina/7/COMB.seq:*
- 9: /EMC_Celerra_SIDS3/prodata/2/ina/RE/COMB.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	70.3	1116	3	US-08-872-485-1
2	26	70.3	1116	3	US-09-387-942-1
3	23	62.2	1734	3	US-09-799-451-243
4	21	56.8	62873	3	US-09-949-016-15676
5	21	56.8	222452	3	US-09-949-016-12968
6	20.8	56.2	1022	3	US-09-257-584-5
7	20.8	56.2	1023	3	US-09-257-584-4
8	20.8	56.2	2546	3	US-09-598-401C-95
9	20.2	54.6	601	3	US-09-949-016-35388
10	20.2	54.6	601	3	US-09-949-016-35389
11	20.2	54.6	601	3	US-09-949-016-44447
12	20.2	54.6	601	3	US-09-949-016-44448
13	20.2	54.6	679	3	US-09-533-559-5172
14	20.2	54.6	50810	3	US-09-949-016-16039
15	20.2	54.6	54452	3	US-09-949-016-12642
16	20.2	54.6	54452	3	US-09-949-016-13003
17	20.2	54.6	60465	3	US-09-949-016-15995
18	20.2	54.1	590	3	US-09-533-559-2554
19	20.2	54.1	601	3	US-09-949-016-84389
20	20.2	54.1	601	3	US-09-949-016-84390
21	20.2	54.1	18798	3	US-09-949-016-17531
22	20.2	54.1	59158	3	US-09-949-002-728
23	20.2	54.1	64994	3	US-09-949-002-688

C	24	20	54.1	94618	4	US-09-531-120-191	Sequence 191, App
C	25	20	54.1	94987	3	US-09-949-016-12510	Sequence 12510, A
C	26	20	54.1	105210	3	US-09-949-016-14158	Sequence 14158, A
C	27	20	54.1	786431	3	US-09-751-389-3	Sequence 3, Appl1
C	28	19.8	53.5	507	3	US-09-621-976-18901	Sequence 18901, A
C	29	19.6	53.0	252	3	US-09-513-999C-28576	Sequence 28576, A
C	30	19.6	53.0	1116	3	US-08-872-485-3	Sequence 3, Appl1
C	31	19.6	53.0	1116	3	US-08-387-942-3	Sequence 3, Appl1
C	32	19.6	53.0	19446	3	US-08-961-527-51	Sequence 51, Appl1
C	33	19.6	53.0	68444	3	US-09-949-016-13968	Sequence 13968, A
C	34	19.6	53.0	107827	3	US-09-949-016-15790	Sequence 15790, A
C	35	19.6	53.0	265038	3	US-09-949-016-15779	Sequence 15779, A
C	36	19.4	52.4	601	3	US-09-949-016-34056	Sequence 34056, A
C	37	19.4	52.4	601	3	US-09-949-016-34057	Sequence 34057, A
C	38	19.4	52.4	601	3	US-09-949-016-140221	Sequence 140221, A
C	39	19.4	52.4	601	3	US-09-949-016-140222	Sequence 140222, A
C	40	19.4	52.4	1389	2	US-08-426-428-1	Sequence 1, Appl1
C	41	19.4	52.4	1389	2	US-08-871-114-1	Sequence 1, Appl1
C	42	19.4	52.4	1838	3	US-09-949-016-261	Sequence 261, App
C	43	19.4	52.4	1838	3	US-09-949-016-1435	Sequence 1435, App
C	44	19.4	52.4	1838	4	US-09-880-107-3813	Sequence 3813, App
C	45	19.4	52.4	1899	3	US-09-919-039-153	Sequence 153, App

ALIGNMENTS

RESULT 1
US-08-872-485-1
Sequence 1, Application US/08872485
Patent No. 6096529
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Young, N. Martin
APPLICANT: Jennings, Michael P.
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases
TITLE OF INVENTION: and Their Uses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,485
FILING DATE: 07-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,520
FILING DATE: 10-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 014137-012000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:

ORGANISM: Neisseria meningitidis
STRAIN: 406Y, NRCC 4030
INDIVIDUAL ISOLATE: Capsule type: Y; lipooligosaccharide
INDIVIDUAL ISOLATE: type: L3
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1116
OTHER INFORMATION: /product= "alpha-2,3-sialyltransferase"
US-08-872-485-1

Query Match 70.3%; Score 26; DB 3; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAAAAGCTTTGACC 37
DB 2 TGGGCTTGAAAAAGCTTTGACC 27

RESULT 2

US-09-387-942-1
Sequence 1, Application US/09387942
Patent No. 6210933

GENERAL INFORMATION:

APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Young, N. Martin
TITLE OF INVENTION: Jennings, Michael P.
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,942
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/872,485
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 014137-012000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Neisseria meningitidis
STRAIN: 406Y, NRCC 4030
INDIVIDUAL ISOLATE: Capsule type: Y; lipooligosaccharide
INDIVIDUAL ISOLATE: type: L3
NAME/KEY: CDS
LOCATION: 1..1116
OTHER INFORMATION: /product= "alpha-2,3-sialyltransferase"

US-09-387-942-1

Query Match 70.3%; Score 26; DB 3; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAAAAGCTTTGACC 37
DB 2 TGGGCTTGAAAAAGCTTTGACC 27

RESULT 3

US-09-799-451-243
Sequence 243, Application US/09799451
Patent No. 6783969

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yundong
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhi-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
TITLE OF INVENTION: Dmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_Fl_genes Version 2.0
SEQ ID NO 243
LENGTH: 1734
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (208) ..(1695)
US-09-799-451-243

Query Match 62.2%; Score 23; DB 3; Length 1734;
Best Local Similarity 83.9%; Pred. No. 7.4;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGAATTCGGGCTTGAAAAAGCTTTGA 35
DB 589 GAATTCGGGCTTTAAAAAGACTTGCTGA 619

RESULT 4

US-09-949-016-15676/c
Sequence 15676, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-3-10-20
PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15676
LENGTH: 62873
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) .. (62873)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15676

Query Match 56.8%; Score 21; DB 3; Length 62873;
Best Local Similarity 82.8%; Pred. No. 1e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 AATTCTGGGCTTGAAAAAGCTTGTGA 35
DB 44328 AATTATGGGCTTGAAAAAGTTTATGA 44300

RESULT 5
US-09-949-016-12968/c
Sequence 12968, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12968
LENGTH: 222452
TYPE: DNA
ORGANISM: Human
US-09-949-016-12968

Query Match 56.8%; Score 21; DB 3; Length 222452;
Best Local Similarity 82.8%; Pred. No. 1.3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TGAATCTGGGCTTGAAAAAGCTTGT 32
DB 84712 TGAATCTGGTGTGAAAAAGTCTGT 84664

RESULT 6
US-09-257-584-5
Sequence 5, Application US/09257584A
Patent No. 6177611
GENERAL INFORMATION:
APPLICANT: Rice, Douglas A.
TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 5718-33, 035718/175218
CURRENT APPLICATION NUMBER: US/09/257,584A
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/076,075
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5

LENGTH: 1022
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: efla-15 promoter
US-09-257-584-5

Query Match 56.2%; Score 20.8; DB 3; Length 1022;
Best Local Similarity 78.1%; Pred. No. 53;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 GGAATCTGGGCTTGAAAAAGCTTGTGAC 36
DB 106 GGAGTTATGAGCTTGAAAAAGCTTGATACAC 137

RESULT 7
US-09-257-584-4
Sequence 4, Application US/09257584A
Patent No. 6177611
GENERAL INFORMATION:
APPLICANT: Rice, Douglas A.
TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 5718-33, 035718/175218
CURRENT APPLICATION NUMBER: US/09/257,584A
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: 60/076,075
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1023
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: efla-11 promoter
US-09-257-584-4

Query Match 56.2%; Score 20.8; DB 3; Length 1023;
Best Local Similarity 78.1%; Pred. No. 53;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 GGAATCTGGGCTTGAAAAAGCTTGTGAC 36
DB 105 GGAGTTATGAGCTTGAAAAAGCTTGATACAC 136

RESULT 8
US-09-598-401C-95/c
Sequence 95, Application US/09598401C
Patent No. 6596925
GENERAL INFORMATION:
APPLICANT: Pereyra, J. Ranjan
APPLICANT: Eagleton, Clare
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.1036c2
CURRENT APPLICATION NUMBER: US/09/598,401C
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 95
LENGTH: 2546
TYPE: DNA
ORGANISM: Pinus radiata
US-09-598-401C-95

Query Match 56.2%; Score 20.8; DB 3; Length 2546;
Best Local Similarity 78.1%; Pred. No. 64;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GCATGAATTCGGCTTGAAAAAGCTTGT 33
DB 1189 CTTGATTCAGTCTGTGAAAAAGCTTGT 1158

RESULT 9
US-09-949-016-35388

/ Sequence 35388, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35388
/ LENGTH: 601

/ TYPE: DNA
/ ORGANISM: Human

US-09-949-016-35388

Query Match 54.6%; Score 20.2; DB 3; Length 601;
Best Local Similarity 75.8%; Pred. No. 85;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCTTGT 33
DB 273 GCATGAATTCCTGTGTGAAAAAGCTTATAT 305

RESULT 10

US-09-949-016-35389

/ Sequence 35389, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35389
/ LENGTH: 601

/ TYPE: DNA
/ ORGANISM: Human

US-09-949-016-35389

Query Match 54.6%; Score 20.2; DB 3; Length 601;
Best Local Similarity 75.8%; Pred. No. 85;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCTTGT 33
DB 118 GCATGAATTCCTGTGTGAAAAAGCTTATAT 150

RESULT 11

US-09-949-016-44447

/ Sequence 44447, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 44447
/ LENGTH: 601

/ TYPE: DNA
/ ORGANISM: Human

US-09-949-016-44447

Query Match 54.6%; Score 20.2; DB 3; Length 601;
Best Local Similarity 75.8%; Pred. No. 85;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCTTGT 33
DB 273 GCATGAATTCCTGTGTGAAAAAGCTTATAT 305

RESULT 12

US-09-949-016-44448

/ Sequence 44448, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 44448
/ LENGTH: 601

/ TYPE: DNA
/ ORGANISM: Human

US-09-949-016-44448

Query Match 54.6%; Score 20.2; DB 3; Length 601;
Best Local Similarity 75.8%; Pred. No. 85;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GCATGAATTCGGCTTGAAAAAGCTTGT 33
DB 118 GCATGAATTCCTGTGTGAAAAAGCTTATAT 150


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RESULT 13
; US-09-533-559-5172/c
; Sequence 5172, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849 200-us
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 1999-03-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5172
; LENGTH: 679
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; US-09-533-559-5172

Query Match      54.6%; Score 20.2; DB 3; Length 679;
Best Local Similarity 75.8%; Pred. No. 87;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      3 ATGGAATTCGGGCTTGAAGGCTTGTGA 35
Db      134 ATAGCATTCCTGCTTGAAGCGGCTGTGGA 102

RESULT 14
; US-09-949-016-16039/c
; Sequence 16039, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16039
; LENGTH: 50810
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16039

Query Match      54.6%; Score 20.2; DB 3; Length 50810;
Best Local Similarity 88.0%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 ATGGAATTCGGGCTTGAAGGCTTGTGA 27
Db      26480 AGGGAATTTGGGCTTGAAGAGGC 26456

RESULT 15
; US-09-949-016-12642
; Sequence 12642, Application US/09949016
; Patent No. 6812339
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12642
; LENGTH: 54452
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12642

Query Match      54.6%; Score 20.2; DB 3; Length 54452;
Best Local Similarity 75.8%; Pred. No. 2.1e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 GCATGGAATTCGGGCTTGAAGGCTTGT 33
Db      43064 GCATGGAATTCCTGTGTTGAAGAGCTTATAT 43096

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Job time : 61.3542 secs
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Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 04:17:10 ; Search time 637.094 Seconds

(without alignments)
713.619 Million cell updates/sec

Title: US-09-211-691-5

Perfect score: 37
Sequence: 1 gcatagaattctggccttgaaagagctgttgacc 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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- 8: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/Ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	37	US-09-211-691-5	Sequence 5, Appl1
2	37	100.0	37	US-10-317-773-5	Sequence 5, Appl1
3	37	100.0	37	US-10-317-428-5	Sequence 5, Appl1
4	26.4	71.4	16878	US-10-915-740A-62	Sequence 62, Appl1
5	26.4	71.4	2242716	US-10-915-740A-1068	Sequence 1068, Appl1
6	24.4	65.9	598	US-10-750-185-19677	Sequence 19677, A
7	24.4	65.9	598	US-10-750-623-19677	Sequence 19677, A
8	24.4	65.9	795	US-10-750-185-29101	Sequence 29101, A
9	24.4	65.9	795	US-10-750-623-29101	Sequence 29101, A
10	24.4	65.9	1386	US-10-437-963-88295	Sequence 88295, A
11	24.4	65.9	1752	US-10-437-963-88295	Sequence 88295, A
12	24.4	65.9	460	US-10-027-632-34789	Sequence 88327, A
13	24.2	65.4	460	US-10-027-632-34789	Sequence 34789, A
14	23.2	62.3	2613	US-11-097-143-25837	Sequence 25837, A
15	22.8	61.6	1734	US-10-302-172-243	Sequence 243, App
16	22.8	61.6	560	US-09-925-065A-542557	Sequence 542557, A
17	22.8	61.6	560	US-09-925-065A-542557	Sequence 542557, A

18	22.8	61.6	584	US-10-437-963-88306	Sequence 88306, A
19	22.8	61.6	5848	US-10-017-161-1659	Sequence 1659, App
20	22.6	61.1	3773	US-10-108-260A-841	Sequence 841, App
21	21.8	58.9	369	US-09-925-065A-123503	Sequence 123503, A
22	21.8	58.9	369	US-09-925-065A-123503	Sequence 123503, A
23	21.8	58.9	377	US-10-301-480-221380	Sequence 221380, A
24	21.8	58.9	377	US-10-301-480-834789	Sequence 834789, A
25	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
26	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
27	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
28	21.8	58.9	523	US-09-925-065A-16964	Sequence 16964, A
29	21.8	58.9	523	US-10-301-480-118201	Sequence 118201, A
30	21.8	58.9	523	US-10-301-480-118202	Sequence 118202, A
31	21.8	58.9	523	US-10-301-480-731610	Sequence 731610, A
32	21.8	58.9	523	US-10-301-480-731611	Sequence 731611, A
33	21.8	58.9	614	US-10-301-480-250004	Sequence 250004, A
34	21.8	58.9	614	US-10-301-480-863413	Sequence 863413, A
35	21.8	58.9	621	US-09-925-065A-156805	Sequence 156805, A
36	21.8	58.9	621	US-09-925-065A-156805	Sequence 156805, A
37	21.6	58.4	854	US-10-425-115-3254	Sequence 3254, App
38	21.6	58.4	1096	US-10-425-114-17871	Sequence 17871, A
39	21.6	58.4	1180	US-10-425-114-35457	Sequence 35457, A
40	21.6	58.4	1256	US-10-425-115-39969	Sequence 39969, A
41	21.6	58.4	1277	US-10-425-115-39967	Sequence 39967, A
42	21.6	58.4	2017	US-10-450-763-16289	Sequence 16289, A
43	21.6	58.4	2165	US-10-450-763-4449	Sequence 4449, App
44	21.4	57.8	482	US-10-301-480-16119	Sequence 16119, A
45	21.4	57.8	482	US-10-301-480-629528	Sequence 629528, A

ALIGNMENTS

RESULT 1
US-09-211-691-5
Sequence 5, Application US/09211691
Patent No. US20020034805A1
GENERAL INFORMATION:
APPLICANT: Gilibert, Michel
APPLICANT: Young, N. Martin
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Fusion Proteins for Use in Enzymatic Synthesis of
FILE REFERENCE: 019957-012910US
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: US 60/069,443
PRIOR FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 37
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:SIAM-22F 5'
OTHER INFORMATION: primer
US-09-211-691-5
Query Match 100.0%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATGAATTCTGGCCTTGAAAGAGCTGTTGACC 37
DB 1 GCATGAATTCTGGCCTTGAAAGAGCTGTTGACC 37
RESULT 2
US-10-317-773-5
Sequence 5, Application US/1031773
Publication No. US20030180928A1

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/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ TITLE OF INVENTION: National Research Council of Canada
/ TITLE OF INVENTION: Fusion Protein Comprising a UDP-GalNac 4' Epimerase and a
/ FILE REFERENCE: 019633-000812US
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 37
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIALM-22F 5'
US-10-317-773-5
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Query Match          100.0%; Score 37; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
DB      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
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RESULT 3
US-10-317-428-5
/ Sequence 5, Application US/10317428
/ Publication No. US20030186414A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ TITLE OF INVENTION: National Research Council of Canada
/ TITLE OF INVENTION: Nucleic Acid That Encodes a Fusion Protein
/ FILE REFERENCE: 019633-000811US
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR FILING DATE: 2002-12-11
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 37
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIALM-22F 5'
US-10-317-428-5
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Query Match          100.0%; Score 37; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
DB      1 GCATGGAATTCCTGGCGCTTGAAAAAGCGTTGTTGACC 37
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RESULT 4
US-10-915-740A-62/C
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/ Sequence 62, Application US/10915740A
/ Publication No. US20050191316A1
/ GENERAL INFORMATION:
/ APPLICANT: Frazer, Claire M.
/ APPLICANT: Hickey, Erin
/ APPLICANT: Peterson, Jeremy
/ APPLICANT: Tettelin, Hervé
/ APPLICANT: Venter, J. Craig
/ APPLICANT: Masiagnani, Vega
/ APPLICANT: Galeotti, Cesira
/ APPLICANT: Mora, Manroza
/ APPLICANT: Ratti, Giulio
/ APPLICANT: Scarselli, Maria
/ APPLICANT: Scariato, Vincenzo
/ APPLICANT: Rappuoli, Rino
/ APPLICANT: Pizsa, Mariagratia
/ APPLICANT: Grandi, Guido
/ TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
/ FILE REFERENCE: 002441.00090
/ CURRENT FILING DATE: 2004-08-11
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR FILING DATE: 1999-10-08
/ NUMBER OF SEQ ID NOS: 1068
/ SOFTWARE: Patent In version 3.2
/ SEQ ID NO 62
/ LENGTH: 16878
/ TYPE: DNA
/ ORGANISM: Neisseria meningitidis
US-10-915-740A-62

Query Match          71.4%; Score 26.4; DB 10; Length 16878;
Best Local Similarity 96.4%; Pred. No. 3.6;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      10 TCTGGCTTGAAAAAGCGTTGTTGACC 37
DB      5806 TATGGCTTGAAAAAGCGTTGTTGACC 5779
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RESULT 5
US-10-915-740A-1068
/ Sequence 1068, Application US/10915740A
/ Publication No. US20050191316A1
/ GENERAL INFORMATION:
/ APPLICANT: Frazer, Claire M.
/ APPLICANT: Hickey, Erin
/ APPLICANT: Peterson, Jeremy
/ APPLICANT: Tettelin, Hervé
/ APPLICANT: Venter, J. Craig
/ APPLICANT: Masiagnani, Vega
/ APPLICANT: Galeotti, Cesira
/ APPLICANT: Mora, Manroza
/ APPLICANT: Ratti, Giulio
/ APPLICANT: Scarselli, Maria
/ APPLICANT: Scariato, Vincenzo
/ APPLICANT: Rappuoli, Rino
/ APPLICANT: Pizsa, Mariagratia
/ APPLICANT: Grandi, Guido
/ TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
/ FILE REFERENCE: 002441.00090
/ CURRENT FILING DATE: 2004-08-11
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR FILING DATE: 1999-10-08
/ PRIOR FILING DATE: 1998-10-09
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PRIOR APPLICATION NUMBER: USSN 60/132,068
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/US99/25373
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 1068
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1068
LENGTH: 2242716
TYPE: DNA
ORGANISM: Neisseria meningitidis
US-10-915-740A-1068

Query Match 71.4%; Score 26.4; DB 10; Length 2242716;
Best Local Similarity 96.4%; Pred. No. 10;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TCTGGCCTGAAAAGCCTGTTGACC 37
DB 934750 TATGGCCTGAAAAGCCTGTTGACC 934777

RESULT 6
US-10-750-185-19677
Sequence 19677, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19677
LENGTH: 598
TYPE: DNA
ORGANISM: Bovine MMBT06634
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(69)
OTHER INFORMATION: n is any nucleotide
US-10-750-185-19677

Query Match 65.9%; Score 24.4; DB 10; Length 598;
Best Local Similarity 82.4%; Pred. No. 12;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATGAATTCGGGCTGAAAAGCCTGTTGA 35
DB 81 CATGAATGCTGGGCTTGAGAAATGCTGATT 114

RESULT 7
US-10-750-623-19677
Sequence 19677, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19677
LENGTH: 598
TYPE: DNA
ORGANISM: Bovine MMBT06634
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(69)
OTHER INFORMATION: n is any nucleotide
US-10-750-623-19677

Query Match 65.9%; Score 24.4; DB 10; Length 598;
Best Local Similarity 82.4%; Pred. No. 12;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATGAATTCGGGCTGAAAAGCCTGTTGA 35
DB 81 CATGAATGCTGGGCTTGAGAAATGCTGATT 114

RESULT 8
US-10-750-185-29101
Sequence 29101, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29101
LENGTH: 795
TYPE: DNA
ORGANISM: Bovine 19866880610988
US-10-750-185-29101

Query Match 65.9%; Score 24.4; DB 10; Length 795;
Best Local Similarity 82.4%; Pred. No. 13;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CATGAATTCGGGCTGAAAAGCCTGTTGA 35
DB 12 CATGAATGCTGGGCTTGAGAAATGCTGATT 45

RESULT 9
US-10-750-623-29101
Sequence 29101, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis

```

; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: M11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29101
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Bovine 19866880610988
US-10-437-963-29101

```

```

Query Match      65.9%; Score 24.4; DB 10; Length 795;
Best Local Similarity 82.4%; Pred. No. 13;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

QY 2 CATGAATTCGGGCTTGAAGGCTTTGAC 35
DB 12 CATGAATGCTGGCTTGAAGGCTTTGAC 45

```

```

RESULT 10
US-10-437-963-88295
; Sequence 88295, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 88295
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8715C.1
US-10-437-963-88295

```

```

Query Match      65.9%; Score 24.4; DB 8; Length 1386;
Best Local Similarity 82.4%; Pred. No. 14;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

QY 4 TGAATTCGGGCTTGAAGGCTTTGAC 37
DB 532 TGAATTCGGGCTTGAAGGCTTTGAC 565

```

```

RESULT 11
US-10-437-963-88327
; Sequence 88327, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

```

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 88327
; LENGTH: 1752
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8718C.1
US-10-437-963-88327

```

```

Query Match      65.9%; Score 24.4; DB 8; Length 1752;
Best Local Similarity 82.4%; Pred. No. 15;
Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

QY 4 TGAATTCGGGCTTGAAGGCTTTGAC 37
DB 838 TGAATGAGGACTTGAAGGCTTTGAC 871

```

```

RESULT 12
US-10-027-632-34789
; Sequence 34789, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34789
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(460)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-34789

```

```

Query Match      65.4%; Score 24.2; DB 6; Length 460;
Best Local Similarity 89.7%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2 CATGAATTCGGGCTTGAAGGCTTTG 30
DB 44 CATGAATTCCTGGCTAGAAAAAGCTTG 72

```

```

RESULT 13
US-10-027-632-34789
; Sequence 34789, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34789
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(460)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-34789
```

```
Query Match 65.4%; Score 24.2; DB 7; Length 460;
Best Local Similarity 89.7%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 CATGAAATTCGGCTGAAAAAGCTTG 30
Db 44 CATGAAATTCCTGGCTGAAAAAGCTTG 72
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RESULT 14
US-11-097-143-25837/C
; Sequence 25837, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25837
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; LENGTH: 2613
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-25837
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Query Match 62.7%; Score 23.2; DB 13; Length 2613;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY 1 GCATGAAATTCGGCTGAAAAAGCTTGTTCAC 36
Db 2436 GCATGAAATTCGGCTTTCAGGCTTGTTCAC 2401
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RESULT 15
US-10-302-172-243
; Sequence 243, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
```

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; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 803_1CNCB
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pc_FL_genes Version 2.0
; SEQ ID NO 243
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (208)..(1695)
US-10-302-172-243
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Query Match 62.2%; Score 23; DB 8; Length 1734;
Best Local Similarity 83.9%; Pred. No. 57;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 5 GCAATTCGGCTGAAAAAGCTTGTTCAC 35
Db 589 GCAATTCGGCTTAAAAAGACTTGTTCAC 619
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OM nucleic - nucleic search, using sw model

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Title: US-09-211-691-5

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Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications NA New:*

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7: /EMC_Celerra_SIDS3/prodata/2/pubphn/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/prodata/2/pubphn/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	56.8	699	US-11-217-529-5602	Sequence 5602, Ap
2	19.6	53.0	4263	US-11-327-900-5	Sequence 5, Appl1
3	19.4	52.4	1904	US-10-505-928-546	Sequence 546, App
4	18.8	50.8	3243	US-10-528-032-8	Sequence 8, Appl1
5	18.8	50.8	3586	US-10-528-032-10	Sequence 10, Appl1
6	18.6	50.3	882	US-11-217-529-2683	Sequence 2683, Ap
7	18.6	50.3	2154	US-11-217-529-173201	Sequence 173201, Ap
8	18.6	50.3	2169	US-11-217-529-4118	Sequence 4118, Ap
9	18.6	50.3	2781	US-10-511-937-470	Sequence 470, App
10	18.6	50.3	3856	US-11-217-529-2801	Sequence 2801, App
11	18.2	49.2	1689	US-10-505-928-208	Sequence 208, App
12	18.2	49.2	2499	US-11-217-529-4580	Sequence 4580, Ap
13	18.2	49.2	2522	US-11-246-999-12	Sequence 12, Appl
14	18.2	49.2	2522	US-11-246-999-23	Sequence 23, Appl
15	18.2	49.2	2565	US-11-217-529-1739	Sequence 1739, App
16	18.2	49.2	12783	US-11-217-529-4700	Sequence 4700, Ap
17	18	48.6	852	US-11-217-529-76150	Sequence 76150, A
18	18	48.6	1371	US-11-217-529-76850	Sequence 76850, A
19	18	48.6	1899	US-11-217-529-77023	Sequence 77023, A
20	17.8	48.1	852	US-11-217-529-80619	Sequence 80619, A
21	17.8	48.1	1602	US-11-217-529-4421	Sequence 4421, App
22	17.8	48.1	2870	US-10-505-928-204	Sequence 204, App
23	17.8	48.1	3780	US-10-511-937-2811	Sequence 2811, App
24	17.8	48.1	4887	US-11-217-529-2955	Sequence 2955, Ap
25	17.6	47.6	1176	US-11-217-529-5552	Sequence 5552, Ap

26	17.6	47.6	1410	7	US-11-217-529-2085	Sequence 2085, Ap
27	17.6	47.6	1896	7	US-11-217-529-78791	Sequence 78791, A
28	17.4	47.0	1951	7	US-11-217-529-173771	Sequence 173771, A
29	17.4	47.0	1233	7	US-11-217-529-1345	Sequence 1345, Ap
30	17.4	47.0	1545	7	US-11-217-529-80280	Sequence 80280, A
31	17.4	47.0	1590	7	US-11-217-529-77057	Sequence 77057, A
32	17.4	47.0	2484	6	US-10-488-619-2017	Sequence 2017, Ap
33	17.4	47.0	2484	7	US-11-217-529-5651	Sequence 5651, Ap
34	17.2	46.5	606	7	US-11-217-529-81626	Sequence 81626, A
35	17.2	46.5	1098	7	US-11-217-529-4515	Sequence 4515, Ap
36	17.2	46.5	1278	7	US-11-217-529-1053	Sequence 1053, Ap
37	17.2	46.5	1320	7	US-11-217-529-1053	Sequence 1053, Ap
38	17.2	46.5	2163	7	US-11-217-529-190821	Sequence 190821, Ap
39	17.2	46.5	3591	7	US-11-217-529-190890	Sequence 190890, Ap
40	17.2	46.5	4816	7	US-11-217-529-190890	Sequence 190890, Ap
41	17.2	46.5	5251	7	US-11-217-529-190899	Sequence 190899, Ap
42	17.2	46.5	5269	7	US-11-217-529-190913	Sequence 190913, Ap
43	17.2	46.5	5269	7	US-11-217-529-190944	Sequence 190944, Ap
44	17.2	46.5	5269	7	US-11-217-529-191008	Sequence 191008, Ap
45	17.2	46.5	5269	7	US-11-217-529-191008	Sequence 191008, Ap

ALIGNMENTS

```

RESULT 1
US-11-217-529-5602/c
; Sequence 5602, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5602
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5602

Query Match      56.8%; Score 21; DB 7; Length 699;
Best Local Similarity 82.8%; Pred. No. 1.5;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 CATGGAATCTCGGCTTGAAAAAGCTTG 30
DB      531 CATGGAATCTCGTATTAAGATAGCATG 503

RESULT 2
US-11-327-900-5
; Sequence 5, Application US/11327900
; Publication No. US20060099174A1
; GENERAL INFORMATION:
; APPLICANT: PHARMA PACIFIC
; APPLICANT: Merileet, Jean Francois
; APPLICANT: Dron, Michel
; APPLICANT: Tovey, Michael Gerard
; TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE
; FILE REFERENCE: 46658/250044
; CURRENT APPLICATION NUMBER: US/11/327,900
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/203,311

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;; PRIOR FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: GB 0002979.3
;; PRIOR FILING DATE: 2000-02-09
;; PRIOR APPLICATION NUMBER: GB 0002980.1
;; PRIOR FILING DATE: 2000-02-09
;; PRIOR APPLICATION NUMBER: GB 0002982.7
;; PRIOR FILING DATE: 2000-02-09
;; PRIOR APPLICATION NUMBER: GB 0002981.9
;; PRIOR FILING DATE: 2000-02-09
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 5
;; LENGTH: 4263
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(3705)
US-11-327-900-5

Query Match
Best Local Similarity 53.0%; Score 19.6; DB 7; Length 4263;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GCATGAATTCGTGGCTGGAAGG 26
DB 771 GCATGAATTCGTGGCTGGAAGG 796

RESULT 3
US-10-505-928-546
;; Sequence 546, Application US/10505928
;; Publication No. US20060088532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ludwig Institute for Cancer Research et al.
;; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;; FILE REFERENCE: 28967/39178
;; CURRENT APPLICATION NUMBER: US/10/505,928
;; PRIOR FILING DATE: 2004-08-27
;; PRIOR APPLICATION NUMBER: US 60/363,019
;; PRIOR FILING DATE: 2002-03-07
;; NUMBER OF SEQ ID NOS: 866
;; SOFTWARE: PatentIn 3.2
;; SEQ ID NO 546
;; LENGTH: 1904
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-505-928-546

Query Match
Best Local Similarity 52.4%; Score 19.4; DB 6; Length 1904;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 GCATGAATTCGTGGCTGGAAGGCTTTGAC 37
DB 476 GCATGAATTCGTGGCTGGAAGGCTTTGAC 512

RESULT 4
US-10-528-032-8
;; Sequence 8, Application US/10528032
;; Publication No. US20060101530A1
;; GENERAL INFORMATION:
;; APPLICANT: EXELIXIS, INC.
;; TITLE OF INVENTION: RORS AS MODIFIERS OF THE P21 PATHWAY AND METHODS OF USE
;; FILE REFERENCE: EX03-068C-US
;; CURRENT APPLICATION NUMBER: US/10/528,032
;; PRIOR FILING DATE: 2005-03-16
;; PRIOR APPLICATION NUMBER: US 60/411,010
;; PRIOR FILING DATE: 2002-09-16
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 8

;; LENGTH: 3243
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-528-032-8

Query Match
Best Local Similarity 50.8%; Score 18.8; DB 6; Length 3243;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4 TGAATTCGTGGCTGGAAGGCTTTGTT 33
DB 2906 TGAATTCGTGGCTGGAAGGCTTTGTT 2935

RESULT 5
US-10-528-032-10
;; Sequence 10, Application US/10528032
;; Publication No. US20060101530A1
;; GENERAL INFORMATION:
;; APPLICANT: EXELIXIS, INC.
;; TITLE OF INVENTION: RORS AS MODIFIERS OF THE P21 PATHWAY AND METHODS OF USE
;; FILE REFERENCE: EX03-068C-US
;; CURRENT APPLICATION NUMBER: US/10/528,032
;; PRIOR FILING DATE: 2005-03-16
;; PRIOR APPLICATION NUMBER: US 60/411,010
;; PRIOR FILING DATE: 2002-09-16
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 10
;; LENGTH: 3586
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-528-032-10

Query Match
Best Local Similarity 50.8%; Score 18.8; DB 6; Length 3586;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4 TGAATTCGTGGCTGGAAGGCTTTGTT 33
DB 2941 TGAATTCGTGGCTGGAAGGCTTTGTT 2970

RESULT 6
US-11-217-529-2683
;; Sequence 2683, Application US/11217529
;; Publication No. US20060099612A1
;; GENERAL INFORMATION:
;; APPLICANT: SUNTORY LIMITED
;; APPLICANT: NAKAO, YOSHIHIRO
;; APPLICANT: NAKAMURA, NORIHIISA
;; APPLICANT: KODAMA, YUKIKO
;; APPLICANT: FUJIMURA, TOMOKO
;; APPLICANT: ASHIKAWA, TOSHIHIKO
;; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;; FILE REFERENCE: S-38-285
;; CURRENT APPLICATION NUMBER: US/11/217,529
;; PRIOR FILING DATE: 2005-09-02
;; PRIOR APPLICATION NUMBER: US 10/932,182
;; PRIOR FILING DATE: 2004-09-02
;; NUMBER OF SEQ ID NOS: 197023
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 2683
;; LENGTH: 882
;; TYPE: DNA
;; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2683

Query Match
Best Local Similarity 50.3%; Score 18.6; DB 7; Length 882;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 ATTCTGGCTTGAAAGGCTTGT 32

Db 634 ATTAGAGCTGAAAAAGCTTGT 658

RESULT 7

US-11-217-529-173201
; Sequence 173201, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173201
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173201

Query Match 50.3%; Score 18.6; DB 7; Length 2154;

Best Local Similarity 84.0%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 TGGGCTTGAAGGCTTGTGAC 36
Db 1302 TGAGCTTGAAGGCTTGTGAC 1326

RESULT 8

US-11-217-529-4118
; Sequence 4118, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4118
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4118

Query Match 50.3%; Score 18.6; DB 7; Length 2169;

Best Local Similarity 72.7%; Pred. No. 21;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 ATGAATTCGGGCTTGAAGGCTTGTGA 35
Db 863 ATGAATTCGGGCTTGAAGGCTTGTGA 895

RESULT 9

US-10-511-937-470/c
; Sequence 470, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fey, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 470
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-470

Query Match 50.3%; Score 18.6; DB 6; Length 2781;

Best Local Similarity 72.7%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GCATGGAATTCGGGCTTGAAGGCTTGT 33
Db 1498 GCTTAGAATTCGGGCTTGAAGGCTTGT 1466

RESULT 10

US-11-217-529-2801/c
; Sequence 2801, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2801
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2801

Query Match 50.3%; Score 18.6; DB 7; Length 2868;

Best Local Similarity 72.7%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 GGAATTCGGGCTTGAAGGCTTGTGACC 37
Db 684 GGAATTCGGGCTTGAAGGCTTGTGACC 652

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RESULT 11
US-10-505-928-208
; Sequence 208, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28667/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 208
; LENGTH: 3856
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-208
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Query Match          50.3%; Score 18.6; DB 6; Length 3856;
Best Local Similarity 72.7%; Pred. No. 24;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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OY 5 GGAATTCTGGGCTTGAAGGCTTTTGACC 37
DB 1694 GTAATCTGTGCTTGACAAAGGAGATTCTCC 1726
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RESULT 12
US-11-217-529-4580/c
; Sequence 4580, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 4580
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4580
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Best Local Similarity 74.2%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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DB 690 ATCGAAATCGTCGATTGACAGGCTTGT 660
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RESULT 13
US-11-246-999-12/c
; Sequence 12, Application US/11246999
; Publication No. US20060099622A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
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; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 2499
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-246-999-12
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Best Local Similarity 74.2%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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OY 4 TGAATCTGGGCTTGAAGGCTTTTG 34
DB 2123 TGGCATTTGGGCTGCGATTAATTCCTTTTG 2093
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RESULT 14
US-11-246-999-23/c
; Sequence 23, Application US/11246999
; Publication No. US20060099622A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 23
; LENGTH: 2522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-246-999-23
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Query Match          49.2%; Score 18.2; DB 7; Length 2522;
Best Local Similarity 74.2%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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OY 4 TGAATCTGGGCTTGAAGGCTTTTG 34
DB 2133 TGGCATTTGGGCTGCGATTAATTCCTTTTG 2103
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RESULT 15
US-11-217-529-1739/c
; Sequence 1739, Application US/11217529
; Publication No. US20060099612A1
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; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1739
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-1739

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Query Match          49.2%; Score 18.2; DB 7; Length 2565;
Best Local Similarity 74.2%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      5 GGAATTCGGGCTGAAAAAGCTTGTTCGA 35
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DB      1007 GTAATCTGGGGGTTTAAAAATGTGTTTTCGA 977

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Search completed: May 19, 2006, 04:25:03
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TITLE Moxon,E.Richard.
JOURNAL Recombinant .alpha.-2,3-sialyltransferases and their uses
FEATURES Patent: US 6210933-A 6 03-APR-2001;
source location/Qualifiers
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Query Match 63.4%; Score 37.4; DB 2; Length 63;
Best Local Similarity 87.2%; Pred. No. 0.0011;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 1 CCTAGTGCACCTCATTAGTGTGATGGTGTGATGGTTCAGGCTTC 47

RESULT 3
LOCUS BD009737 63 bp DNA linear PAT 31-JAN-2002
DEFINITION Recombinant alpha-2,3-sialyltransferases and their uses.
ACCESSION BD009737
VERSION BD009737.1 GI:18638110
KEYWORDS JP 2001503961-A/6.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 63)
AUTHORS Gilbert,M., Wakarchuk,W.W., Young,M.N. and Jennings,M.P.
TITLE Recombinant alpha-2,3-sialyltransferases and their uses
JOURNAL Patent: JP 2001503961-A 6 27-MAR-2001;
NATIONAL RESEARCH COUNCIL OF CANADA
COMMENT OS unidentified
PN JP 2001503961-A/6
PD 27-MAR-2001
PF 10-JUN-1997 JP 1997526320
PR

PI MICHEL GILBERT, WARREN W WAKARCHUK, MARTIN N YOUNG, PI MICHAEL P JENNINGS
PC C12N15/54, C12N15/70, C12N15/79, C12N9/10, C12N5/10, C12N1/21, PC C12P19/26
CC Strandedness: Single;
CC Topology: Linear;
CC Key
FH Key
FT source
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location/Qualifiers
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FEATURES
source location/Qualifiers
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ORIGIN

Query Match 63.4%; Score 37.4; DB 2; Length 63;
Best Local Similarity 87.2%; Pred. No. 0.0011;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCTAGTGCACCTCATTAGTGTGATGGTGTGATGGTTCAGGCTTC 47
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Db 1 CCTAGTGCACCTCATTAGTGTGATGGTGTGATGGTTCAGGCTTC 47

RESULT 4
LOCUS BD134501 60 bp DNA linear PAT 18-SEP-2002
DEFINITION Lipopolysaccharide alpha-2,3 sialyltransferase of Campylobacter jejuni and its uses.
ACCESSION BD134501
VERSION BD134501.1 GI:23229446
KEYWORDS JP 2002507424-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct

other sequences; artificial sequences.
1 (bases 1 to 60)
AUTHORS Gilbert,M. and Wakarchuk,W.W.
TITLE Lipopolysaccharide alpha-2,3 sialyltransferase of Campylobacter jejuni and its uses
JOURNAL Patent: JP 2002507424-A 3 12-MAR-2002;
NATIONAL RESEARCH COUNCIL OF CANADA
COMMENT OS Artificial Sequence
PN JP 2002507424-A/3
PD 12-MAR-2002
PF 22-MAR-1999 JP 2000538012
PR 20-MAR-1998 US 60/078891, 18-MAR-1999 US 09/272960 PI MICHEL GILBERT, WARREN W WAKARCHUK
PC C12N15/09, C12N1/21, C12N5/10, C12N9/10, C12P19/26, C12N15/00, C12N5/10
CC Description of Artificial Sequence: C140R 3' primer FH Key
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FT 1..60
location/Qualifiers
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FEATURES
source location/Qualifiers
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ORIGIN

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Best Local Similarity 85.1%; Pred. No. 0.005;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCTAGTGCACCTCATTAGTGTGATGGTGTGATGGTTCAGGCTTC 47
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Db 1 CCTAGTGCACCTCATTAGTGTGATGGTGTGATGGTTCAGGCTTC 47

RESULT 5
LOCUS AR473909 60 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 4 from patent US 6689604.
ACCESSION AR473909
VERSION AR473909.1 GI:42712448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 60)
AUTHORS Gilbert,M. and Wakarchuk,W.W.
TITLE Lipopolysaccharide .alpha.-2,3 sialyltransferase of Campylobacter jejuni and its uses
JOURNAL Patent: US 6689604-A 4 10-FEB-2004;
NATIONAL RESEARCH COUNCIL OF CANADA; Ottawa, CAN;
COMMENT

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ORIGIN

Query Match 60.7%; Score 35.8; DB 2; Length 60;
Best Local Similarity 85.1%; Pred. No. 0.005;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 1 CCTAGTGCACCTCATTAGTGTGATGGTGTGATGGTTCAGGCTTC 47

RESULT 6
LOCUS AR489132 60 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 4 from patent US 6709834.
ACCESSION AR489132

VERSION AR489132.1 GI:47256034
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 60)
AUTHORS Gilbert,M. and Makarchuk,W.W.
TITLE Lipopolyaccharide .alpha.-2,3 sialyltransferase of campylobacter jejuni and its uses
JOURNAL Patent: US 6709834-A 4 23-MAR-2004;
National Research Council of Canada, Ottawa;
CAX;
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 60.7%; Score 35.8; DB 2; Length 60;
Best Local Similarity 85.1%; Pred. No. 0.005; 7; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CCTAGTCGACTCATTTAGTGTGATGGTGTGATGTTTCAGTCTTC 47
1 CCTAGTCGACTCATTTAGTGTGATGGTGTGATGTTCCCTTCTC 47
Db

RESULT 7
LOCUS AR393465 1149 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6617115.
ACCESSION AR393465
VERSION AR393465.1 GI:40120036
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1149)
AUTHORS Wood,K.W., Finer,J.T., Beraud,C., Mak,J. and Sakowicz,R.
TITLE Methods of screening for modulators of cell proliferation
JOURNAL Patent: US 6617115-A 3 09-SEP-2003;
Cytokinetix, Inc.; South San Francisco, CA
FEATURES
source Location/Qualifiers
1..1149
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 59.7%; Score 35.2; DB 2; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.0053; 8; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 12 TCATTAGTGTGATGGTGTGATGTTTCAGTCTTCTTCGCTGATCAG 59
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RESULT 8
LOCUS AR393466 1542 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6617115.
ACCESSION AR393466
VERSION AR393466.1 GI:40120038
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1542)
AUTHORS Wood,K.W., Finer,J.T., Beraud,C., Mak,J. and Sakowicz,R.
TITLE Methods of screening for modulators of cell proliferation
JOURNAL Patent: US 6617115-A 5 09-SEP-2003;
Cytokinetix, Inc.; South San Francisco, CA
FEATURES
Location/Qualifiers

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ORIGIN
Query Match 59.7%; Score 35.2; DB 2; Length 1542;
Best Local Similarity 83.3%; Pred. No. 0.005; 8; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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12 TCATTAGTGTGATGGTGTGATGTTTCAGTCTTCTTCGCTGATCAG 1495
Db 1542 TCATTAGTGTGATGGTGTGATGTTTCAGTCTTCTTCGCTGATCAG 1495

RESULT 9
LOCUS AR224042 1569 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6440684.
ACCESSION AR224042
VERSION AR224042.1 GI:23332661
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Beraud,C., Finer,J.T., Sakowicz,R. and Wood,K.W.
TITLE Methods of identifying modulators of kinesin motor proteins
JOURNAL Patent: US 6440684-A 3 27-AUG-2002;
Cytokinetix, Inc.; South San Francisco, CA
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source Location/Qualifiers
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 0.005; 8; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 10
LOCUS AR393467 1728 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6617115.
ACCESSION AR393467
VERSION AR393467.1 GI:40120040
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1728)
AUTHORS Wood,K.W., Finer,J.T., Beraud,C., Mak,J. and Sakowicz,R.
TITLE Methods of screening for modulators of cell proliferation
JOURNAL Patent: US 6617115-A 7 09-SEP-2003;
Cytokinetix, Inc.; South San Francisco, CA
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 59.7%; Score 35.2; DB 2; Length 1728;
Best Local Similarity 83.3%; Pred. No. 0.0049; 8; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 12 TCATTAGTGTGATGGTGTGATGTTTCAGTCTTCTTCGCTGATCAG 59
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Db 1728 TCATTAGTGTGATGGTGTGATGTTTCAGTCTTCTTCGCTGATCAG 1681

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ORIGIN
Query Match 57.3%; Score 33.8; DB 8; Length 530;
Best Local Similarity 84.4%; Pred. No. 0.023;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY
15 TTAGTGTGATGGTGTGATGTTTCAGTCTTTCGCTGATCAG 59
Db 474 TCACATATGATGATGATGATGTTTCAGATCTTTCGCTGATCAG 430

RESULT 14
AJ619719/c
LOCUS
DEFINITION
AJ619719 530 bp DNA linear SYN 19-FEB-2004
Expression vector pVT2 synthetic gene for pentavalent protein 2
precursor.
AJ619719.1 GI:41411189
pentavalent protein 2.
Expression vector pVT2
Expression vector pVT2
Other sequences; artificial sequences; vectors.
1
Zhang, J. and Mackenzie, R.
Plasmid vectors for the construction of pentavalent proteins
unpublished
2 (bases 1 to 530)
Zhang, J.
Direct Submission
Submitted (16-DEC-2003) Zhang J., Institute for Biological
Sciences, National Research Council, 100 Sussex Dr., Ottawa,
Ontario, K1A 0R6, CANADA
Location/Qualifiers
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136..468
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/experiment="experimental evidence, no additional details recorded"

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136..468
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Best Local Similarity 84.4%; Pred. No. 0.023;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY
15 TTAGTGTGATGGTGTGATGTTTCAGTCTTTCGCTGATCAG 59
Db 474 TCACATATGATGATGATGATGTTTCAGATCTTTCGCTGATCAG 430

RESULT 15
AJ619720/c
LOCUS
DEFINITION
AJ619720 530 bp DNA linear SYN 19-FEB-2004
Expression vector pVT3 synthetic gene for pentavalent protein 3
precursor.
AJ619720.1 GI:41411191
pentavalent protein 3.
Expression vector pVT3
Expression vector pVT3
Other sequences; artificial sequences; vectors.
1
Zhang, J. and Mackenzie, R.
Plasmid vectors for the construction of pentavalent proteins
unpublished
2 (bases 1 to 530)
Zhang, J.
Direct Submission
Submitted (16-DEC-2003) Zhang J., Institute for Biological
Sciences, National Research Council, 100 Sussex Dr., Ottawa,
Ontario, K1A 0R6, CANADA
Location/Qualifiers
1..530
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/db_xref="taxon:262222"
73..471
/experiment="experimental evidence, no additional details recorded"

CDS
1..530
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/protein_id="CAF22055.1"
/db_xref="GI:41411192"
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KVEYTKYNDDEDTFVKVGDKELPFNRNKLSLLSAQITGMVTITKTNCHNGGGRSE
VIRGGGGSLAGSEOKLISEBDLNHHHH"
73..135
/experiment="experimental evidence, no additional details recorded"

sig_peptide
/note="ompa leader"
136..468
/product="pentavalent protein 3 precursor"
/experiment="experimental evidence, no additional details recorded"

mat_peptide
136..468
/product="pentavalent protein 3 precursor"
/experiment="experimental evidence, no additional details recorded"

ORIGIN
Query Match 57.3%; Score 33.8; DB 8; Length 530;
Best Local Similarity 84.4%; Pred. No. 0.023;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY
15 TTAGTGTGATGGTGTGATGTTTCAGTCTTTCGCTGATCAG 59
Db 474 TCACATATGATGATGATGATGTTTCAGATCTTTCGCTGATCAG 430

Fri May 19 11:37:23 2006

us-09-211-691-6.rge

Page 6

Search completed: May 19, 2006, 01:27:34
Job time : 1259.67 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 22:50:10 ; Search time 282.094 Seconds
(without alignments)
1458.248 Million cell updates/sec

Title: US-09-211-691-6

Perfect score: 59
Sequence: 1 cccagtcgacatcatcgtg.....aggctcttcgcgcgcacag 59

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_8:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2002bs:*
9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	59	2	AAx84285
2	37.4	63.4	63	2	AAV04130
3	35.8	60.7	60	2	AAZ25695
4	35.2	59.7	1149	4	AAc85781
5	35.2	59.7	1542	4	AAc85782
6	35.2	59.7	1569	6	ABSS5161
7	35.2	59.7	1728	4	AAc85783
8	33.8	57.3	867	2	AAV10119
9	33.8	57.3	867	4	AAAD04539
10	33.8	57.3	867	4	AAAD04540
11	33.8	57.3	867	9	ACA62170
12	33.8	57.3	867	12	ADOS2300
13	33.8	57.3	867	12	ADOS2298
14	33.8	57.3	885	6	ABK97798
15	33.8	57.3	918	2	AAV10118
16	33.8	57.3	918	4	AAAD04537
17	33.8	57.3	918	4	AAAD04538
18	33.8	57.3	918	9	ACA62168

C	19	33.8	57.3	918	12	ADOS2295	Ados2295 Human ant
C	20	33.8	57.3	918	12	ADOS2297	Ados2297 Human ant
C	21	33.8	57.3	1152	6	ABK97808	Abk97808 DNA encod
C	22	33.8	57.3	3604	6	ABK97805	Abk97805 Interfero
C	23	33.6	56.9	206	2	AAV81221	Aav81221 Plasmid p
C	24	33	55.9	72	2	AAV72070	Aav72070 806.077 s
C	25	33	55.9	72	2	AAV72071	Aav72071 806.077 s
C	26	32.2	54.6	2013	6	ABU59152	Abu59152 Sequence
C	27	31.2	52.9	88	6	ABN84817	Abn84817 Human DNA
C	28	29.2	49.5	3093	10	ADD14876	Add14876 Phage d18
C	29	29	49.2	705	9	ADB85116	Adb85116 TNF fusio
C	30	29	49.2	1806	6	ABA99914	Ab999914 TNF-selec
C	31	29	49.2	1806	6	ABL61057	Ab161057 TNF-selec
C	32	29	49.2	1906	6	ADD13791	Add13791 Plasmid p
C	33	29	49.2	1977	6	ABA99913	Ab999913 TNF-selec
C	34	28.8	48.8	888	14	ADZ66383	Adz66383 MOFI ant
C	35	28.8	48.8	898	2	AAV73335	Aav73335 Mouse OKT
C	36	28.8	48.8	1653	3	AAZ43432	Aaz43432 Fv-antibo
C	37	28.8	48.8	1698	3	AAZ43431	Aaz43431 Fv-antibo
C	38	28.8	48.8	1794	2	AAV73337	Aav73337 Mouse bis
C	39	28.8	48.8	1817	8	ACC79606	Acc79606 Plasmid p
C	40	28.8	48.8	1817	8	ACC79607	Acc79607 Plasmid p
C	41	28.8	48.8	1897	10	ADE29201	Ade29201 Multivale
C	42	28.8	48.8	4570	4	AAE61152	Aae61152 Single ch
C	43	28.4	48.1	1574	3	AAZ57599	Aaz57599 Erythrocy
C	44	28	47.5	70	15	ABG11345	Aeg11345 P. falci
C	45	27.4	46.4	72	2	AAZ21147	Aaz21147 C-myc pep

ALIGNMENTS

RESULT 1
AAx84285
ID AAX84285 standard; DNA; 59 BP.
XX
AC AAX84285;
XX
DT 08-SEP-1999 (first entry)
XX
XX PCR primer for alpha-2,3-sialyltransferase coding sequence.
DE
XX Beta-1,4-galactosyltransferase; lgtB; fusion protein; catalytic domain;
KW glycosyltransferase; accessory enzyme; nucleotide sugar formation;
KW saccharide donor; oligosaccharide synthesis; alpha-2,3-sialyltransferase;
KW carbohydrate structure development; PCR primer; ss.
XX
XX Synthetic.
OS Neisseria sp.
XX
XX W099931224-AA2.
XX
PD 24-JUN-1999.
XX
PF 15-DEC-1998; 98WO-CA001180.
XX
XX 15-DEC-1997; 97US-0069443P.
XX 14-DEC-1998; 98US-00211691.
XX
XX (CANA) NAT RES COUNCIL CANADA.
XX
PI Gilbert M, Young NM, Wakarchuk WW;
XX WPI; 1999-395174/33.
XX
XX A new glycosyltransferase fusion protein useful in the enzymatic
PT synthesis of oligosaccharides.
XX
XX Example 1; Page 40; 63pp; English.
XX
XX This sequence represents a PCR primer for the Neisseria alpha-2,3-
CC sialyltransferase coding sequence. The invention relates to a nucleic
CC acid encoding a fusion protein that comprises a glycosyltransferase

CC catalytic domain and a catalytic domain from an accessory enzyme that is
 CC involved in formation of a nucleotide sugar which is a saccharide donor
 CC for a glycosyltransferase reaction. The fusion protein is useful in the
 CC enzymatic synthesis of oligosaccharides. The fusion proteins are able to
 CC catalyze more than one reaction involved in the enzymatic synthesis. This
 CC is useful for the development of therapeutic agents that have specific
 CC carbohydrate structures. Carbohydrates are involved in recognition
 CC elements on the surface of cells. The fusion protein can be used for the
 CC synthesis of both natural carbohydrates and synthetic derivatives with
 CC novel properties. The fusion polypeptide allows two glycosyltransferase
 CC reactions in a single vessel, provides improved yields of end products.
 CC Additionally, cleanup and disposal of extra solvents and by-products is
 CC reduced. The fusion protein can also use directly different donor
 CC analogues and various acceptors with a terminal galactose residue
 CC
 SQ Sequence 59 BP; 9 A; 11 C; 19 G; 20 T; 0 U; 0 Other;

Query Match
 Best Local Similarity 100.0%; Score 59; DB 2; Length 59;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTAGTGCATCTATTAGTGTGATGGTGGATGCTTCAGTCTTCTTCGCTGATCAG 59
 DB 1 CCTAGTGCATCTATTAGTGTGATGGTGGATGCTTCAGTCTTCTTCGCTGATCAG 59

RESULT 2

AAV04130
 ID AAV04130 standard; DNA; 63 BP.

AC AAV04130;

DT 17-JUN-1998 (first entry)

DE Neisseria sp. alpha-2,3-sialyltransferase PCR primer SIALM-17R.

KM alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid; PCR primer;
 KM biologically active oligosaccharide; sialyl-modified protein; ss.

OS Synthetic.
 OS Neisseria meningitidis.

PN MO9747749-A1.

PD 18-DEC-1997.

PF 10-JUN-1997; 97WO-CA000390.

PR 10-JUN-1996; 96US-0019520P.

PR 07-JUN-1997; 97US-00872485.

PA (CANA) NAT RES COUNCIL CANADA.

PI Gilbert M, Makarchuk WW, Young NM, Jennings MP;

DR WPI; 1998-052313/05.

PT Nucleic acid sequence encoding Neisseria alpha-2,3-sialyltransferase -
 PT useful to add sialic acid to acceptor with terminal galactose residue for
 PT synthesis of biologically active oligosaccharide.

PS Example 2; Page 25; 50pp; English.

CC AAV01427-001430 are PCR primers used in the amplification of novel alpha-
 CC 2,3-sialyltransferase from Neisseria meningitidis and Neisseria
 CC gonorrhoeae. The protein can be used as a reagent for adding a sialic acid
 CC residue to an acceptor having a terminal galactose residue, e.g. in
 CC synthesis of biologically active oligosaccharides or sialyl-modified
 CC proteins or lipids. The nucleic acid sequence can be used for the
 CC recombinant production of alpha-2,3-sialyltransferase

SQ Sequence 63 BP; 15 A; 9 C; 18 G; 21 T; 0 U; 0 Other;

Query Match
 Best Local Similarity 63.4%; Score 37.4; DB 2; Length 63;
 Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CCTAGTGCATCTATTAGTGTGATGGTGGATGCTTCAGTCTTCTTCGCTGATCAG 47
 DB 1 CCTAGTGCATCTATTAGTGTGATGGTGGATGCTTCAGTCTTCTTCGCTGATCAG 47

RESULT 3

AAZ25695
 ID AAZ25695 standard; DNA; 60 BP.

AC AAZ25695;

DT 05-JAN-2000 (first entry)

DE Campylobacter jejuni alpha-2,3-sialyltransferase PCR primer CJ40R.

KM Campylobacter jejuni; alpha-2,3-sialyltransferase; cst-I; acceptor;
 KM lipopolysaccharide; galactose residue; sialic acid molecule; PCR primer;
 ss.

OS Synthetic.

OS Campylobacter jejuni.

PN MO9949051-A1.

PD 30-SEP-1999.

PF 22-MAR-1999; 99WO-CA000238.

PR 20-MAR-1998; 98US-0078891P.

PR 18-MAR-1999; 99US-00272960.

PA (CANA) NAT RES COUNCIL CANADA.

PI Gilbert M, Makarchuk WW;

DR WPI; 1999-601216/51.

PT New sialyltransferases useful for adding sialyl residues to acceptor
 PT molecules.

PS Disclosure; Page 14; 47pp; English.

CC The present sequence represents a PCR primer for the Campylobacter jejuni
 CC cst-I gene which encodes alpha-2,3-sialyltransferase. The alpha-2,3-
 CC sialyltransferase protein is useful for producing desired carbohydrate
 CC structures by contacting the acceptor molecule (which has a terminal
 CC galactose residue) with an activated sialic acid molecule. The terminal
 CC galactose residue is linked to a second residue (Glc or a GlcNAc, or
 CC GlcNAc or GalNAc) in the acceptor molecule through a beta-1,3 or beta-1,4
 CC linkage, respectively. The activated sialic acid is CMP-Neu5Ac. The
 CC polynucleotides and polypeptides facilitate the improved production of
 CC desired structures and nucleic acids encoding sialyltransferases

SQ Sequence 60 BP; 9 A; 17 C; 13 G; 21 T; 0 U; 0 Other;

Query Match
 Best Local Similarity 60.7%; Score 35.8; DB 2; Length 60;
 Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CCTAGTGCATCTATTAGTGTGATGGTGGATGCTTCAGTCTTCTTCGCTGATCAG 47
 DB 1 CCTAGTGCATCTATTAGTGTGATGGTGGATGCTTCAGTCTTCTTCGCTGATCAG 47

RESULT 4

AAAC85781/C
 ID AAC85781 standard; cDNA; 1149 BP.

AC AAC85781;

```

XX 18-JUL-2001 (first entry)
XX DE cDNA encoding KSPJ360.
XX DE Human, kinesin; KSP; drug screening; mitotic spindle; mitosis;
XX KM ATP hydrolysis; apoptosis; necrosis; cancer; ss.
XX OS Synthetic.
XX PN WO200131335-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029570.
XX PR 27-OCT-1999; 99US-00428156.
XX PA (CYTO-) CYTOKINETICS INC.
XX PI Wood KW, Finer JT, Beraud C, Mak J, Sakowicz R;
XX DR WPI; 2001-300550/31.
XX P-PSDB; AAB47213.
XX PT Screening for drug candidates and treating cancer by using kinesin KSP.
XX PS Disclosure; Fig 3; 63pp; English.
XX CC This sequence encodes the kinesin, KSPJ360, which may be used in the
XX CC method of the invention to screen for drug candidates and bioactive
XX CC agents. The method comprises combining the candidate and a cell
XX CC expressing recombinant KSP, and determining the effect of the candidate
XX CC on the bioactivity of recombinant KSP. Changes in the bioactivity of KSP
XX CC spindle, particularly inhibition of mitosis, and ATP hydrolysis. It may
XX CC also be determined by performing assays to determine the effect of
XX CC candidate agents on apoptosis and necrosis. The method of the invention
XX CC is useful for screening for drug candidates (especially bioactive agents
XX CC and proteins) which effect the bioactivity of KSP, binding to KSP and/or
XX CC expression of KSP, where the cells are cancer cells.
XX SQ Sequence 1149 BP; 367 A; 207 C; 269 G; 306 T; 0 U; 0 Other;

Query Match 59.7%; Score 35.2; DB 4; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.087;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 12 TCATTAGTGTGATGCTGATGCTTCCTTCCTGATCAG 59
DB 1149 TCAGTGTGTGCTGCTGCTGATCAGGCTCCTCCTGCTATCAG 1102

RESULT 5
AAC85782/C
ID AAC85782 standard; cDNA; 1542 BP.
XX AC AAC85782;
XX XX 18-JUL-2001 (first entry)
XX DE cDNA encoding KSP-K491.
XX KM Human, kinesin; KSP; drug screening; mitotic spindle; mitosis;
XX KM ATP hydrolysis; apoptosis; necrosis; cancer; ss.
XX OS Synthetic.
XX PN WO200131335-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029570.

```

```

XX 27-OCT-1999; 99US-00428156.
XX PA (CYTO-) CYTOKINETICS INC.
XX PI Wood KW, Finer JT, Beraud C, Mak J, Sakowicz R;
XX DR WPI; 2001-300550/31.
XX P-PSDB; AAB47214.
XX PT Screening for drug candidates and treating cancer by using kinesin KSP.
XX PS Disclosure; Fig 5; 63pp; English.
XX CC This sequence encodes the kinesin, KSP-K491, which may be used in the
XX CC method of the invention to screen for drug candidates and bioactive
XX CC agents. The method comprises combining the candidate and a cell
XX CC expressing recombinant KSP, and determining the effect of the candidate
XX CC on the bioactivity of recombinant KSP. Changes in the bioactivity of KSP
XX CC spindle, particularly inhibition of mitosis, and ATP hydrolysis. It may
XX CC also be determined by performing assays to determine the effect of
XX CC candidate agents on apoptosis and necrosis. The method of the invention
XX CC is useful for screening for drug candidates (especially bioactive agents
XX CC and proteins) which effect the bioactivity of KSP, binding to KSP and/or
XX CC expression of KSP, where the cells are cancer cells.
XX SQ Sequence 1542 BP; 528 A; 257 C; 354 G; 403 T; 0 U; 0 Other;

Query Match 59.7%; Score 35.2; DB 4; Length 1542;
Best Local Similarity 83.3%; Pred. No. 0.091;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 12 TCATTAGTGTGATGCTGATGCTTCCTTCCTGATCAG 59
DB 1542 TCAGTGTGTGCTGCTGCTGATCAGGCTCCTCCTGCTATCAG 1495

RESULT 6
ABSS5161/C
ID ABSS5161 standard; DNA; 1569 BP.
XX AC ABSS5161;
XX XX 10-DEC-2002 (first entry)
XX DE Human Hskif4 construct gene.
XX KM Microtubule stimulated ATPase; cellular proliferation; cancer; AIDS;
XX KM hyperplasia; restenosis; cardiac hypertrophy; immune disorder; HIV;
XX KM inflammatory bowel disease; arthritis; graft rejection; psoriasis;
XX KM inflammatory bowel disease; proliferation; medical procedure; surgery;
XX KM human immunodeficiency virus; acquired immunodeficiency syndrome;
XX KM angioplasty; human, Hskif4; kinesin family; gene; de.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT CDS
XX FT 1..1569
XX FT Location/Qualifiers
XX FT /*tag= a
XX FT /product= "Human Hskif4 construct protein"
XX FT 1..64
XX FT /*tag= b
XX FT /note= "Encodes N-terminal T7 epitope"
XX FT 1486..1548
XX FT /*tag= c
XX FT /note= "Encodes C-terminal myc epitope"
XX FT 1549..1566
XX FT /*tag= d
XX FT /note= "Encodes 6-histidine residues at C-terminus"
XX PN US6440684-B1.

```

BR	27-OCT-1999;	99US-00428156.
FA	(CYTO-) CYTOKINETICS INC.	
XX		
PI	Wood KM, Finer JT, Beraud C, Mak J, Sakowicz R;	
DR	WPI; 2001-300550/31.	
DR	P-PSDB; AAB47215.	
XX		
PT	Screening for drug candidates and treating cancer by using kinesin K	
XX		
PS	Disclosure; Fig 7; 63bp; English.	
XX		
CC	This sequence encodes the kinesin, KSP-S553, which may be used in the	
CC	method of the invention to screen for drug candidates and bioactive	
CC	agents. The method comprises combining the candidate and a cell	
CC	expressing recombinant KSP, and determining the effect of the candidate	
CC	on the bioactivity of recombinant KSP. Changes in the bioactivity of	
CC	may be determined by assays for determining changes in the mitotic	
CC	spindle, particularly by inhibiting of mitosis, and ATP hydrolysis. It	
CC	also be determined by performing assays to determine the effect of	
CC	candidate agents on apoptosis and necrosis. The method of the invention	
CC	is useful for screening for drug candidates (especially bioactive agents	
CC	and proteins) which effect the bioactivity of KSP, binding to KSP and	
CC	expression of KSP, where the cells are cancer cells	
XX		
SO	Sequence 1728 BP; 594 A; 291 C; 393 G; 450 T; 0 U; 0 Other;	
	Query Match	
	Best Local Similarity 59.7%; Score 35.2; DB 4; Length 1728;	
	Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps	
OY	12 TCATTAGCGTGATGCTGCTGATGCTTCAGGCTTCTTCGCTGATCAG 59	
Db	1728 TCAGTGGTGCTGGTGCTGATGCTTCAGTCTCTCCTCGCTGATCAG 1681	
RESULT 8		
ID	AAV10119/c	
XX	AAV10119 standard; DNA; 867 BP.	
XX		
AC	AAV10119;	
XX		
DT	29-MAY-1998 (first entry)	
XX		
DE	Human H11-scfv construct dimer forming DNA sequence.	
XX		
KW	H11: monoclonal antibody; Mb; C-antigen; variable region heavy chain	
KW	V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe	
KW	primer; vaccine; gene therapy; glioblastoma; neuroblastoma;	
KW	malignant melanoma; adenocarcinoma; small cell lung carcinoma;	
XX	single chain variable region; scfv; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
FH		
FT	Key	Location/Qualifiers
FT	CDS	1..867
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FT		/product= "H11-scfv construct"
FT		/note= "partial sequence of dimer forming construct is
FT	intron	interrupted by an intron."
FT		856..861
FT		/*tag= b
XX		
XX		
XX	MO9744461-A2.	
PN		
PD	27-NOV-1997.	
XX		
PF	22-MAY-1997;	97WO-US008962.
XX		
XX	22-MAY-1996;	96US-00657449.
XX		


```
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Dan MD, Maiti PK, Kaplan HA;
XX
XX WPI; 1998-018515/02.
DR P-PSDB; AAM40071.
XX
PT Antigen binding fragment from monoclonal antibody, H11 - allows tumour
PT specific detection and treatment of neoplasia.
XX
XX Example 7; Page 94-95; 126pp; English.
XX
CC This sequence encodes a human H11 monoclonal antibody single chain V
CC region fragment (H11-scFv) construct which is capable of forming dimers.
CC This construct is used to determine the ability of H11-scFv antibody
CC fragments to bind specifically to the C-antigen on cancer cells. Such
CC antigen binding fragments may be used for treating a patient with
CC neoplasia. It is especially useful in the detection of lymphomas and
CC leukaemias where the tumour cells bearing the C antigen are circulating
CC in the patients bloodstream. The polynucleotide sequence may be used as a
CC primer or a probe and the encoded protein may be used in a vaccine or for
CC gene therapy. The human monoclonal antibody (MAb), designated H11,
CC specifically recognises cancerous cells. H11 is specific for
CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma
CC
SQ Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;
XX
Query Match 57.3%; Score 33.8; DB 2; Length 867;
Best Local Similarity 84.4%; Pred. No. 0.24;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 15 TTAGTGTGATGGTGTGATGGTTCAGTCTTTCGCTGATCAG 59
DB 861 TCACCTATGATGGATGGATGGATGTTCAAGTCTTTCGCTGATCAG 817

RESULT 9
AAD04539/C
ID AAD04539 standard; DNA; 867 BP.
XX
AC AAD04539;
XX
XX 04-JUL-2001 (first entry)
XX
DE Human monoclonal antibody H11-single chain variable region (scFv) DNA #2.
XX
KW Human, monoclonal antibody; Mab; H11; single chain variable region; scFv;
KW neoplastic disease; melanoma; immunoglobulin Igm; gene therapy; lymphoma;
KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
KW C-antigen; chronic leukaemia; glioma; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..867
FT CDS
FT /tag= a
FT /product= "Human H11-single chain variable region (scFv)"
FT /transl_except= (pos:853..864, aa:His-Lys)
FT /note= "Insertion of two inframe stop codon alters the
FT reading frame; CDS does not include start and stop
FT codons"
FT /partial
XX
XX US6207153-B1.
XX
XX 27-MAR-2001.
XX
XX 22-MAY-1997; 97US-00862124.
XX
XX 22-MAY-1996; 96US-00657449.
XX
XX 22-MAY-1996; 96US-00657449.
XX
XX
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XX
XX (VIVE-) VIVENTIA BIOTECH INC.
XX
XX Dan MD, Maiti PK, Kaplan HA;
XX
XX WPI; 2001-289584/30.
DR P-PSDB; AAE00948.
XX
XX Composition comprising antigen binding fragments of an antibody that
XX recognizes an antigen on neoplastic cells but not on normal cells for use
XX in diagnosis, imaging and treatment of carcinomas.
XX
XX Example 7; Col 67-70; 56pp; English.
XX
XX The present DNA sequence encodes human monoclonal antibody (Mab), H11-
XX single chain variable region (scFv). The H11 light chain variable region
XX is linked to the heavy chain variable region through a (SGGGG)3 linker to
XX form dimers. The invention relates to human monoclonal antibody (Mab)
XX H11, H11-(scFv) single chain variable (V) region fragment and their
XX corresponding DNA molecules. H11 antibody is an immunoglobulin of Igm
XX subclass which is specific to C-antigen found specifically on neoplastic
XX cells and not on normal cells. H11 is an antibody obtained from the
XX fusion of peripheral blood lymphocytes of a 64 year old male with a low
XX grade glioma and fused to a human myeloma cell line to produce a
XX hybridoma designated NBGM1/H11. A pharmaceutical composition comprising
XX H11 and its derivatives are useful in the diagnosis, imaging and
XX treatment of neoplastic disease, particularly, melanoma, breast
XX carcinoma, lung carcinoma, ovarian carcinoma, colon carcinoma, gastric
XX carcinoma, prostate carcinoma, lymphoma carcinoma, neuroblastoma, glioma,
XX soft tissue sarcoma, small cell lung carcinoma, prostatic adenocarcinoma,
XX B and T cell lymphomas and chronic leukaemias. H11 DNA is also used in
XX vaccines and gene therapy
XX
SQ Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 U; 0 Other;
XX
Query Match 57.3%; Score 33.8; DB 4; Length 867;
Best Local Similarity 84.4%; Pred. No. 0.24;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 15 TTAGTGTGATGGTGTGATGGTTCAGTCTTTCGCTGATCAG 59
DB 861 TCACCTATGATGGATGGATGGATGTTCAAGTCTTTCGCTGATCAG 817

RESULT 10
AAD04540
ID AAD04540 standard; DNA; 867 BP.
XX
AC AAD04540;
XX
XX 04-JUL-2001 (first entry)
XX
DE Human H11-single chain variable region (scFv) complementary DNA #2.
XX
KW Human, monoclonal antibody; Mab; H11; single chain variable region; scFv;
KW neoplastic disease; melanoma; immunoglobulin Igm; gene therapy; lymphoma;
KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
KW C-antigen; chronic leukaemia; glioma; ds.
XX
XX Homo sapiens.
OS
XX
XX US6207153-B1.
XX
XX 27-MAR-2001.
XX
XX 22-MAY-1997; 97US-00862124.
XX
XX 22-MAY-1996; 96US-00657449.
XX
XX (VIVE-) VIVENTIA BIOTECH INC.
XX
XX Dan MD, Maiti PK, Kaplan HA;
XX
```


Query	15	TTAGTGGTATGGTGGTATGGTTCAGGCTTCTTCGCTATCAG	59
Db	861	TCACTAATGGTGGTATGGTTCAGATCTTCTCGCTGATCAG	817
<p>RESULT 14</p> <p>ABK97798/c</p> <p>ID ABK97798 standard; DNA; 865 BP.</p> <p>XX AC ABR97798;</p> <p>XX DT 07-OCT-2002 (first entry)</p> <p>XX DE C219scFv DNA sequence.</p> <p>XX KW Cytosarptic; virucide; hepatotropic; antiinflammatory; neuroprotective; immunosuppressive; antiarthritic; cytokine receptor; interferon; IFN; cancer; haematological malignancy; viral infection; hepatitis; human; multiple sclerosis; autoimmune disease; arthritis; ds; gene.</p> <p>XX OS Synthetic.</p> <p>XX PN WO200244197-A2.</p> <p>XX PD 06-JUN-2002.</p> <p>XX PF 30-NOV-2001; 2001WO-CA001701.</p> <p>XX PR 01-DEC-2000; 2000US-00727388.</p> <p>XX PA (FISH/) FISH E N.</p> <p>XX PI Fish EN;</p> <p>XX WI: 2002-547689/58.</p> <p>XX P-PSDB: ABG68848.</p> <p>Cytokine receptor binding peptide construct, in particular interferon receptor binding peptide construct for use as an interferon mimetic,</p>			

COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0065 row: E column: 21
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..718
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR CBA0065E21"
/tissue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR_CBA"
/note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"

ORIGIN
Query Match 48.1%; Score 28.4; DB 13; Length 718;
Best Local Similarity 76.1%; Pred. No. 83;
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 13 CATTAGTGTGATGCTGATGCTGATGCTTCTTCGCTGATCA 58
Db 130 CAATAGTGTGCTGTGCTGTGCTGTCTGCTTATGTCATCA 85

RESULT 5
CL796515/c 746 bp DNA linear GSS 06-AUG-2004
LOCUS OR_CBA0006K21.r OR_CBA Oryza rufipogon genomic clone OR_CBA0006K21
DEFINITION 3', genomic survey sequence.
ACCESSION CL796515
VERSION CL796515.1 GI:51018531
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BRP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 746)
Kim,H., Yu,Y., Wisotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jelty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0006 row: K column: 21
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..746
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"

COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0006 row: K column: 21
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..746
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"

ORIGIN
Query Match 48.1%; Score 28.4; DB 13; Length 746;
Best Local Similarity 76.1%; Pred. No. 84;
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 13 CATTAGTGTGATGCTGATGCTGATGCTTCTTCGCTGATCA 58
Db 203 CAATAGTGTGCTGTGCTGTGCTGTCTGCTTATGTCATCA 158

RESULT 6
AA305848
LOCUS EST177056 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
DEFINITION sequence.
ACCESSION AA305848
VERSION AA305848.1 GI:1958400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 550)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bull,C.J., Lee,N.H., Kirness,E.F., Weinstein,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man,Mai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,B.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Rannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Other ESTs: TH0132309
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
source Location/Qualifiers
1..550
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):160223"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/clone_lib="Jurkat T-cells VI"

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/note="Vector: pBluescript SK-, Site_1: EcoRI, Site_2:
XhoI"
ORIGIN

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Query Match	47.8%	Score 28.2;	DB 1;	Length 550;
Best Local Similarity	80.5%;	Pred. No. 94;		
Matches 33; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

Oy 19 TGGGATGGTGGTATGTTCAAGCTCTTCTGCGATCAG 59
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 496 TGGTGACGATGATGCTGTGTAAGGAGCTTCTCCGTGATCAG 536

RESULT 7	CFI31918	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CFI31918	UI-HF-P00-aws-1-23-0-UI.1	689 bp	mRNA	linear	EST 05-AUG-2003			
	IMAGE:1055846 5',		mRNA sequence.					
CFI31918	CFI31918.1	GI:33214657						
EST.								
	Homo sapiens (human)							

REFERENCE	1 (bases 1 to 689)
AUTHORS	Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
PubMed	8889548
COMMENT	Contact: Soares, MB

Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bentto-soares@iowa.edu
Tissue Procurement: Mary Hendrix
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed By: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/human1.html>
Seq primer: pYX-5.

FEATURES	Location/Qualifiers
source	1. .689

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053846"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH0B (T1 plaque resistant)"
/clone_lib="NH_MGC_215"
/note="Organ: Lung; Vector: pYX-Asc; Site:1: EcoR I;
Site:2: Not I; The library was constructed according
to Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer centered according to a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATGAGCCCA. Tissue was provided by Mary Hendrix."

```

Query March	47.8%	Score 28.2;	DB 5;	Length 689;
Best Local Similarity	80.5%;	Pred. No. 97;		
Matches 33;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
Y 19 TGGTATGATGTGTCATCGTTCCAGGTCCTTCCTGCCTCATAG 59				

Db

514 TGGTACGATGATGCTGGTGAAGGCTTCTTCCCTGATCAG 554

RESULT 8	
CNS04DT1	
LOCUS	CNS04DT1 929 bp DNA
DEFINITION	Tetradon nigriviridis genome survey sequence PUC-Orl end of clone
ACCESSION	103c12 of library G from Tetradon nigriviridis, genomic survey
	sequence.
	113c2144.

ACCESSION	AL286174
VERSION	AL286174.1
KEYWORDS	GI:8024620
SOURCE	GSS; genome survey sequence
ORGANISM	Tetradon nigroviridis

ORGANISM
Tetraodon nigroviridis
Eukarya: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Actinopterygii: Neopterygii: Teleostei: Euteleostei, Neuteleostei
Acanthomorpha: Acanthopterygii: Percomorphi: Tetraodontiformes,
Tetraodontidae, Tetraodontidae: Percomorphi: Tetraodontiformes,
1
Roest Crolius, H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C.
REFERENCE
AUTHORS

TITLE	JOURNAL	PUBMED	REFERENCE
Benrath, A., Fitzmes, C., Wincker, P., Bottier, P., Querier, F., Saurin, W. and Weissbach, J. Estimate of human gene number provided by genome-wide analysis using Terradom nigroviridis DNA sequence	Nat. Genet. 25 (2), 235-238 (2000)	10835645	2

AUTHORS
Rosté Cécilinus, H. Vailion, O. Daalila, C. Ozouf-Costaz, C. Flammes, C. Fischer, C. Bonnaud, L. Billault, A. Quetier, F. Saurin, W. Bernot, A. and Weissenbach, J.
TITLE
Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*
JOURNAL
Genome Res. 10 (7), 939-949 (2000)
PUBLISHED
10899143
REFERENCE
3 (pages 1 to 929)

Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Séquençage :
BP 191 91006 Evry cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read, and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigriviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetradon>.

FEATURES	Location/Qualifiers
source	1. .929

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/organism="Tetracodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="103C12"
/clone_lib="G"
/note="Genoscope sequence ID : COMG103BB06SP1
end : PUC-ori"

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ORIGIN	
Query Match	47.8%;
Best Local Similarity	80.5%;
Matches 33; Conservative	0;
Mismatches	8;
Indels	0;
Gaps	0;

10 ACCTATTAGTGATGTCGTGGTGCAGTTCTTC 50
||| ||| ||| ||| ||| ||| ||| |||
205 ACTCATCAGTGGGATGATGATGATCTCTGGCCTTGTC 245

RESULT	9						
LOCUS	BH742923/c						
DEFINITION	BH742923	585 bp	DNA	linear	GenBank	25-SEP-2002	
ACCESSION	g267d03.g1	BoBue01	Brassica	oleracea	genomic clone	g267d03 5'	
VERSION	g267d03						
KEYWORDS	BH742923.1	GI:16877537					
	GSS.						

SOURCE	Brassica oleracea
ORGANISM	Brassica oleracea
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS	Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Balija,V., Cummins,D.M., Katzenberger,F., King,L., Kirchoff,K., Kuit,R., Miller,R., Muller,S., Nascimeto,L., Pretton,R., Santos,L., Shah,R., Zultavern,T., Dedila,N., Rabinowitz,P.D. and McCombie,W.R.
TITLE	Whole Genome Shotgun Reads from Brassica oleracea (2002b)
JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org Plate: gze7 row: d column: 03 Seq primer: -21univrev Class: shotgun High quality sequence stop: 585.
FEATURES	location/Qualifiers
SOURCE	1..585 /organism="Brassica oleracea" /mol_type="genomic DNA" /db_xref="taxon:3712" /clone="gze7d03" /clone_lib="Bobu01" /note="Vector: M13 for .x reads, pBluescript for .b and .g reads; Site_1: EcoRV; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000D3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA provided by Pablo Rabinowicz (CSHL) and shotgun library prepared in McCombie Lab."
ORIGIN	
Query Match	47.5%; Score 28; DB 11; Length 585;
Best Local Similarity	77.3%; Pred. No. 1.1e+02;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
QY	11 TCATTAAGTGTGATGCTGATGCTGATGCTCAGGCTCTTCTGCTG 54 263 CGCGTGTGCTGCTGCTGCTGCTGCTGATGAGGCGTTATCTCTG 220
RESULT 10	
BH586099/c	794 bp DNA linear GSS 15-DEC-2001
LOCUS	
DEFINITION	BOGS192TR BOGS Brassica oleracea genomic clone BOGS192, genomic survey sequence.
ACCESSION	BH586099
VERSION	BH586099.1 GI:17838557
KEYWORDS	GSS.
SOURCE	Brassica oleracea
ORGANISM	Brassica oleracea
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
AUTHORS	Ayale,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utecherack,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
JOURNAL	15805490
PUBMED	Other GSSs: BOGS192TR
COMMENT	Contact: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

```

Tel.: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
    1..794
        /organism="Brassica oleracea"
        /mol_type="genomic DNA"
        /strain="TO100DH3"
        /db_xref="taxon:3712"
        /clone="BOSI92"
        /clone_1id="BOGS"
        /note="Vector: PHO5; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHO5 using BstXI linkers"

ORIGIN
Query Match          47.5%; Score 28; DB 11; Length 794;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches   34; Conservative      0; Mismatches 10; Indels       0; Gaps     0;

QY         11 CTCATTAGTGTCGATGGTGTGAACCTTCAGCCTTCCTCG 54
           ||| |||| |||||| |||| ||| |||| |
Db         497 CGCGTTGTGTGGTGCTGCCTGCCGTAGAAGCCCTATTCTCTG 454


RESULT 11
BU892293/c              722 bp mRNA linear EST 17-OCT-2002
LOCUS                   BU892293
DEFINITION               Populus petioles CDNA library Populus tremula cdna 5 prime.
ACCESSION                BU892293
VERSION                  BU892293.1 GI:24103358
KEYWORDS                 ESR.
SOURCE                   Populus tremula
ORGANISM                 Populus tremula
                           Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                           Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;
                           rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
REFERENCE                Umeberg P., Bhaleerao R.R., Jansson S. and Steark F.
AUTHORS                  The poplar tree transcriptome: Analysis of expressed sequence tags
TITLE                    from multiple libraries
JOURNAL                  Unpublished (2002)
COMMENT                  Contact: BHALERAO RUPALI R.
                          Umea Plant Science Center
                          Department of Plant Physiology
                          University of Umeaa, 901 87 Umeaa, Sweden
                          Tel.: +46 90 786 5279
                          Fax: +46 90 786 6676
                          Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
Source
    1..722
        /organism="Populus tremula"
        /mol_type="mRNA"
        /db_xref="taxon:113636"
        /tisue type="petioles"
        /clone_lib="Populus petioles CDNA library"

ORIGIN
Query Match          47.1%; Score 27.8; DB 3; Length 722;
Best Local Similarity 82.1%; Pred. No. 1.3e+02;
Matches   32; Conservative      0; Mismatches 7; Indels       0; Gaps     0;

QY         13 CATTAGTGTCATGTCGTGTCACTTTAAGCTCTTCTCG 51
           ||| |||| |||||| |||| ||| |||| |
Db         387 CATAAAGTCGTGTGTGTGTGAAGCTTCCTTAG 349


RESULT 12
DM496361/c            855 bp mRNA linear EST 10-MAR-2005
LOCUS                 DM496361
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DEFINITION	P06IG11.3pr Populus petioles cDNA library Populus tremula cDNA clone P06IG11 5' mRNA sequence.
ACCESSION	DNA96361
VERSION	DNA96361.1 GI:60706551
KEYWORDS	EST.
SOURCE	Populus tremula
ORGANISM	Populus tremula
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid I; Malvidiales; Salicaceae; Salix; Populus. 1 (bases 1 to 855)
AUTHORS	Gierthy,F., Bhalarao,R.R., Umeberg,P., Segerman,B., Nilsson,P., Runner,A.M., Charbonnel,Campaa,L., Lindvall,J.J., Tandre,K., Strauss,S.H., Sundberg,B., Gustafsson.P., Uhlen,M., Bhalarao,R.P., Nilsson,O., Sandberg,G., Karlsson,U., Lundberg,J. and Jansson,S. A Populus EST resource for plant functional genomics Proc.Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004) 1535603
TITLE	JOURNAL PUBMED
COMMENT	Other ESTs: P06IG11, P06IG11.3pr Contact: Bo Segerman Umea Plant Science Center, Department of Plant Physiology Umea University 901 87 Umea, Sweden Tel : +46 90 786 5279 Fax : +46 90 786 6676 Email: bo.segerman@plantphys.umu.se. Location/Qualifiers 1..855 /organism="Populus tremula" /mol_type="mRNA" /db_xref="taxon:113636" /clone="P06IG11" /tissue.type="petioles" /clone_lib="Populus petioles cDNA library"
FEATURES	source
ORIGIN	
Query Match	47.1%; Score 27.8; DB 9; Length 855;
Best Local Similarity	82.1%; Pred.No.1.4e+02;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0	
Oy	13 CATTAGTGTGATGGTGATGCATTCAGCTCCTTCCTCG 51 385 CATAGTGTGTGTTGGTGGTGCGTGCTTGGAAGTCTCCCTTAG 347
Db	
RESULT 13	
CW980355	702 bp DNA linear GSS 28-DEC-2004
LOCUS	KBRH004J00SR KBrH, Brassica rapa HindIII BAC library Brassica rapa subsp. pekinensis genomic clone KBrH004005, genomic survey sequence.
ACCESSION	CW980355
VERSION	CW980355
KEYWORDS	CW980355.1 GI:56811642
SOURCE	GSS.
ORGANISM	Brassica rapa subsp. pekinensis Brassica rapa subsp. pekinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Brassica. Yang,T.J., Kwon,S.U., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Lim,Y.P. and Park,B.S. End sequence of Brassica rapa HindIII BAC library (KBrH). Unpublished (2004) Contact: Beom-Seok Park Brassica Genomics Team National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672 Email: pbeomrda.go.kr BAC end sequence of Brassica rapa sep. pekinensis HindIII BAC clone KBrH04005
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

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Seq primer: M13 Reverse
Class: BAC ends
Location/Qualifiers
1..702
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KB-H004J05"
/tissue_type="young leaves"
/lab_host="E.coli DH10B"
/clone_lib="KBrH, Brassica rapa HindIII BAC library"
/note="Vector: pCU6isBac1; Site 1: HindIII; Brassica rapa ssp. pekinensis inbred line Chifu BAC library (KBrH BAC) is provided by Yong-Pyo Lim."

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Query Match          46.8%; Score 27.6; DB 13; Length 702;
Best Local Similarity 67.2%; Pred. No. 1.5e+02;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      2 CTAGTCGACTCATTTAGTGTGATGCTGATGCTGATGGTTCAGGCCTCTTCGCGTGATCAG 59
Db       82 CGAAGCCGATTGATTGCTGATGCTGAGATGATATGATTCAGATTCCTCTTCATCAG 139

RESULT 14
LOCUS     CT034862/c              923 bp      DNA           linear   GSS 01-NOV-2005
DEFINITION Sus scrofa genomic clone CH242-19E6, genomic survey sequence.
ACCESSION CT034862
VERSION    CT034862.1 GI:78630375
KEYWORDS   GSS.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;
            Sus.
            1 (bases 1 to 923)
            Humphray,S.J., Plumb,R.W. and Durham,J.L.
            Direct Submission
            Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humphray@sanger.ac.uk Unpublished
            This sequence was generated from the T7 end of BAC 19E6. 19E6 is
            part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S__scrofa/.
COMMENT
FEATURES             source
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                    /tissue_type="white blood cells"
                    /note="vector pTABAC1.3_BamHI
                    sex female"

ORIGIN
Query Match          46.8%; Score 27.6; DB 14; Length 923;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      5 GGTCGACTCATTTAGTGTGATGCTGATGCTGATGGTTCAGGCTT 46
Db       820 GGTGTCACAATGCTGATGCTGATGCTGATGCTGATGCTGCTT 779

RESULT 15
LOCUS     CX110631              271 bp      mRNA         linear   EST 03-JUN-2005
DEFINITION CX110631
            271 bp      mRNA         linear   EST 03-JUN-2005
            A normalized whole-life-cycle cDNA library of rice Oryza
            sativa (indica cultivar group).

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sequence.
ACCESSION      CX110631
VERSION        CX110631.1  GI:66923783
KEYWORDS
SOURCE
ORGANISM       Oryza sativa (indica cultivar-group)
               Oryza sativa (indica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
               Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BPP
               clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS        Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D.,
               Han,B., Zhang,Q. and Wang,S.
TITLE          Features of the expressed sequences revealed by a large-scale
               analysis of ESTs from a normalized cDNA library of the elite indica
               rice cultivar Minghui 63
JOURNAL        Plant J. 42 (5), 772-780 (2005)
PUBMED        15918889
COMMENT        Contact: Wang S
               National Key Laboratory of Crop Genetic Improvement
               Huazhong Agricultural University
               Wuhan 430070, China
               Tel: 86-27-87282044
               Fax: 86-27-87287092
               Email: shipingwang@hotmail.com
               Seq primer: T7.
FEATURES
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               Location/Qualifiers
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               /organism="Oryza sativa (indica cultivar-group)"
               /mol_type="mRNA"
               /strain="indica"
               /cultivar="Minghui 63"
               /db_xref="taxon:39946"
               /clone="E1050P21"
               /cissue_type="whole plant"
               /dev_stage="whole-life-cycle"
               /lab_host="E. coli DH10B"
               /clone_1lb="A normalized whole-life-cycle cDNA library of
               rice"
               /note="Vector: pSPORT1, Site_1: SalI; Site_2: NotI; The
               library is constructed based on the strategy of saturation
               hybridization with genomic DNA using rice cultivar Minghui
               63. This library consists of cDNA from 15 directionally
               cloned cDNA libraries constructed with different tissues
               from 9 developmental stages."
ORIGIN
Query Match      46.4%; Score 27.4; DB 8; Length 271;
Best Local Similarity 69.8%; Pred. No. 1.6e+02;
Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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DB               78 TAGATTGATTGTTCTTGTGGTGGTGGTGGTGGATCGGTCGCTTGGCTGA 130
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 01:27:44 ; Search time 94.6458 Seconds
(without alignments)
1166.405 Million cell updates/sec

Title: US-09-211-691-6

Perfect score: 59
Sequence: 1 cccagtcgactcatcagtg.....aggtctcttcgctgacag 59

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6 COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	37.4	63.4	63	US-08-872-485-8	Sequence 8, Appli
2	37.4	63.4	63	US-09-387-942-8	Sequence 8, Appli
3	35.8	60.7	60	US-09-272-960-4	Sequence 4, Appli
4	35.8	60.7	60	US-10-058-636-4	Sequence 4, Appli
5	35.2	59.7	1149	US-09-724-519-3	Sequence 3, Appli
6	35.2	59.7	1149	US-09-592-037-3	Sequence 3, Appli
7	35.2	59.7	1149	US-09-428-1568-3	Sequence 3, Appli
8	35.2	59.7	1542	US-09-724-519-5	Sequence 5, Appli
9	35.2	59.7	1542	US-09-592-037-5	Sequence 5, Appli
10	35.2	59.7	1542	US-09-428-1568-5	Sequence 5, Appli
11	35.2	59.7	1569	US-09-592-054-3	Sequence 3, Appli
12	35.2	59.7	1728	US-09-724-519-7	Sequence 7, Appli
13	35.2	59.7	1728	US-09-592-037-7	Sequence 7, Appli
14	35.2	59.7	1728	US-09-428-1568-7	Sequence 7, Appli
15	33.8	57.3	867	US-08-862-124-16	Sequence 16, Appli
16	33.8	57.3	867	US-08-862-124-16	Sequence 16, Appli
17	33.8	57.3	918	US-08-862-124-13	Sequence 13, Appli
18	33.8	57.3	918	US-08-862-124-15	Sequence 15, Appli
19	33	55.9	72	US-09-423-439-45	Sequence 45, Appli
20	33	55.9	72	US-09-423-439-46	Sequence 46, Appli
21	27.4	46.4	72	US-09-646-028-25	Sequence 25, Appli
22	27.4	46.4	1086	US-09-646-028-39	Sequence 39, Appli
23	27.4	46.4	1086	US-09-646-028-36	Sequence 36, Appli

C 24	27.4	46.4	1113	3	US-09-646-028-38	Sequence 38, Appli
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C 27	26.8	45.4	483	3	US-09-270-767-9516	Sequence 9516, Ap
C 28	26.8	45.4	483	3	US-09-270-767-24798	Sequence 24798, A
C 29	26.8	45.4	711	3	US-09-107-532A-1515	Sequence 1515, Ap
C 30	26.6	45.1	843	3	US-09-423-439-43	Sequence 43, Appli
C 31	26.6	45.1	864	3	US-09-423-439-47	Sequence 47, Appli
C 32	26.6	45.1	1176	3	US-09-826-509-568	Sequence 568, App
C 33	26.6	45.1	1205	2	US-08-417-103-13	Sequence 13, Appli
C 34	26.6	45.1	1634	2	US-07-816-283-1	Sequence 1, Appli
C 35	26.6	45.1	1634	2	US-08-417-103-1	Sequence 1, Appli
C 36	26.6	45.1	1634	2	US-09-016-434-1302	Sequence 1302, Ap
C 37	26.4	44.7	816	3	US-08-643-704A-47	Sequence 47, Appli
C 38	26.4	44.7	1236	3	US-08-643-704A-48	Sequence 48, Appli
C 39	25.8	43.7	699	3	US-09-252-991A-5247	Sequence 5247, Ap
C 40	25.8	43.7	1674	3	US-09-252-991A-5216	Sequence 5216, Ap
C 41	25.4	43.1	1434	3	US-09-252-991A-13254	Sequence 13254, A
C 42	25.4	43.1	1545	3	US-09-252-991A-12705	Sequence 12705, A
C 43	25.4	43.1	1548	3	US-08-668-373-13	Sequence 13, Appli
C 44	25.4	43.1	2172	3	US-09-252-991A-13088	Sequence 13088, A
C 45	25.4	43.1	57280	3	US-09-949-016-11796	Sequence 11796, A

ALIGNMENTS

RESULT 1
US-08-872-485-8
Sequence 8, Application US/08872485
Patent No. 6096529
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Young, N. Martin
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases
TITLE OF INVENTION: and Their Uses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,485
FILING DATE: 07-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,520
FILING DATE: 10-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 014137-012000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

NAME/KEY: -
LOCATION: 1..63
OTHER INFORMATION: /note="5' primer SIALM-17R"
US-08-872-485-8

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Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 2
US-09-387-942-8
Sequence 8, Application US/09387942
Patent No. 6210933
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: Young, N. Martin
APPLICANT: Jennings, Michael P.
TITLE OF INVENTION: Recombinant alpha-2,3-Sialyltransferases
TITLE OF INVENTION: and Their Uses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09387,942
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/872,485
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 014137-012000US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..63
OTHER INFORMATION: /note="5' primer SIALM-17R"
US-09-387-942-8

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Best Local Similarity 87.2%; Pred. No. 0.00082;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 3
US-09-272-960-4
Sequence 4, Application US/09272960
Patent No. 6689604
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
FILE REFERENCE: 014137-013210US
CURRENT APPLICATION NUMBER: US/09/272,960
PRIOR FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 60/078,891
EARLIER FILING DATE: 1998-03-20
EARLIER APPLICATION NUMBER: US 09/272,960
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:CU40R 3' primer
US-09-272-960-4

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Best Local Similarity 85.1%; Pred. No. 0.0029;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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RESULT 4
US-10-058-636-4
Sequence 4, Application US/10058636
Patent No. 6709834
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
FILE REFERENCE: 014137-013210US
CURRENT APPLICATION NUMBER: US/10/058,636
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US/09/272,960
PRIOR FILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/078,891
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/272,960
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:CU40R 3' primer
US-10-058-636-4

Query Match 60.7%; Score 35.8; DB 3; Length 60;
Best Local Similarity 85.1%; Pred. No. 0.0029;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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; Sequence 3, Application US/09724519
; Patent No. 6414121
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; TITLE OF INVENTION: proliferation states
; FILE REFERENCE: 1014A
; CURRENT APPLICATION NUMBER: US/09/724,519
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/592,037
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 09/428,156
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Human
US-09-724-519-3

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Best Local Similarity 83.3%; Pred. No. 0.0094;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db      1149 TCAGTGTGTGATGGTGTGATGATGATTCAGGCTCTTCTTCGCTGATCAG 1102

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US-09-592-037-3/c
; Sequence 3, Application US/09592037
; Patent No. 6437115
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; TITLE OF INVENTION: proliferation states
; FILE REFERENCE: 1014A
; CURRENT APPLICATION NUMBER: US/09/592,037
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 09/428,156
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Human
US-09-592-037-3

Query Match      59.7%; Score 35.2; DB 3; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.0094;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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US-09-428-156B-3/c
; Sequence 3, Application US/09428156B
; Patent No. 6617115
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; TITLE OF INVENTION: proliferation states
; FILE REFERENCE: CYT0P033
; CURRENT APPLICATION NUMBER: US/09/428,156B
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Human
US-09-428-156B-3

Query Match      59.7%; Score 35.2; DB 3; Length 1149;
Best Local Similarity 83.3%; Pred. No. 0.0094;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      12 TCATTAGTGTGATGGTGTGATGATGATTCAGGCTCTTCTTCGCTGATCAG 59
Db      1149 TCAGTGTGTGATGGTGTGATGATGATTCAGGCTCTTCTTCGCTGATCAG 1102

RESULT 8
US-09-724-519-5/c
; Sequence 5, Application US/09724519
; Patent No. 6414121
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth
; APPLICANT: Finer, Jeffrey
; APPLICANT: Beraud, Christophe
; APPLICANT: Mak, John
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Methods of screening for modulators of
; TITLE OF INVENTION: cell proliferation and methods of diagnosing cell
; TITLE OF INVENTION: proliferation states
; FILE REFERENCE: 1014A
; CURRENT APPLICATION NUMBER: US/09/724,519
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 09/592,037
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 09/428,156
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Human
US-09-724-519-5

Query Match      59.7%; Score 35.2; DB 3; Length 1542;
Best Local Similarity 83.3%; Pred. No. 0.01;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      12 TCATTAGTGTGATGGTGTGATGATGATTCAGGCTCTTCTTCGCTGATCAG 59
Db      1542 TCAGTGTGTGATGGTGTGATGATGATTCAGGCTCTTCTTCGCTGATCAG 1495

RESULT 9
US-09-592-037-5/c
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RESULT 11
 US-09-592-054-3/C
 Sequence 3, Application US/09592054
 Patent No. 6440684
 GENERAL INFORMATION:
 APPLICANT: Berard, Christophe
 APPLICANT: Finer, Jeffrey

RESULT 13
US-09-592-037-7/C
Sequence 7, Application US/09592037
Patent No. 6437115
GENERAL INFORMATION:
APPLICANT: Wood, Kenneth
APPLICANT: Finer, Jeffrey
APPLICANT: Beraud, Christophe
APPLICANT: Mak, John
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Methods of screening for modulators of cell proliferation and methods of diagnosing cells

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/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Fusion Protein Comprising a UDP-GalNac 4' Epimerase and a
/ FILE REFERENCE: 019633-000812US
/ CURRENT APPLICATION NUMBER: US/10/317,773
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR APPLICATION NUMBER: US 09/211,691
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 59
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIAM-23R 3'
/ US-10-317-773-6
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Query Match      100.0%; Score 59; DB 7; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 CCTAGTGCAGCTCATTAGTGTGATGCGTGTGATGCTTTCCTTCCTGCATCAG 59
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RESULT 3
US-10-317-428-6
/ Sequence 6, Application US/10317428
/ Publication No. US2003018641A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Young, N. Martin
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Nucleic Acid That Encodes a Fusion Protein
/ FILE REFERENCE: 019633-000811US
/ CURRENT APPLICATION NUMBER: US/10/317,428
/ CURRENT FILING DATE: 2002-12-11
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1997-12-15
/ PRIOR APPLICATION NUMBER: US 09/211,691
/ PRIOR FILING DATE: 1998-12-14
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 59
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:SIAM-23R 3'
/ US-10-317-428-6
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Query Match      100.0%; Score 59; DB 7; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 CCTAGTGCAGCTCATTAGTGTGATGCGTGTGATGCTTTCCTTCCTGCATCAG 59
DB      1 CCTAGTGCAGCTCATTAGTGTGATGCGTGTGATGCTTTCCTTCCTGCATCAG 59
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RESULT 4
US-10-058-636-4
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/ Sequence 4, Application US/10058636
/ Publication No. US20030049270A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
/ FILE REFERENCE: 014137-013210US
/ CURRENT APPLICATION NUMBER: US/10/058,636
/ CURRENT FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: US/09/272,960
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: US 60/078,891
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: US 09/272,960
/ PRIOR FILING DATE: 1999-03-18
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:CT40R 3' primer
/ US-10-058-636-4
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Query Match      60.7%; Score 35.8; DB 6; Length 60;
Best Local Similarity 85.1%; Pred. No. 0.023;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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OY      1 CCTAGTGCAGCTCATTAGTGTGATGCGTGTGATGCTTTCCTTCCTGCATCAG 47
DB      1 CCTAGTGCAGCTCATTAGTGTGATGCGTGTGATGCTTTCCTTCCTGCATCAG 47
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RESULT 5
US-10-799-016-4
/ Sequence 4, Application US/10799016
/ Publication No. US20040152165A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Michel
/ APPLICANT: Makarchuk, Warren W.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
/ FILE REFERENCE: 014137-013210US
/ CURRENT APPLICATION NUMBER: US/10/799,016
/ CURRENT FILING DATE: 2004-03-11
/ PRIOR APPLICATION NUMBER: US/10/058,636
/ PRIOR FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: US 60/078,891
/ PRIOR FILING DATE: 1999-03-18
/ PRIOR APPLICATION NUMBER: US 09/272,960
/ PRIOR FILING DATE: 1999-03-18
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:CT40R 3' primer
/ US-10-799-016-4
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```
Query Match      60.7%; Score 35.8; DB 6; Length 60;
Best Local Similarity 85.1%; Pred. No. 0.023;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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OY      1 CCTAGTGCAGCTCATTAGTGTGATGCGTGTGATGCTTTCCTTCCTGCATCAG 47
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 867
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-651-453-18

Query Match 57.3%; Score 33.8; DB 8; Length 867;
Best Local Similarity 84.4%; Pred. No. 0.18;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 15 TTATGGTATGGTGGTATGATGTTTCAGTCTTTCGCTGATCAG 59
Db 7 TCACATAAGTGATGGTATGGTATGATGTTTCAGATCTTTCGCTGATCAG 51

RESULT 13
US-09-782-397-13/c
Sequence 13, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Mafti, Pradip K.
Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: join(1..306, 913..918)
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-782-397-13

Query Match 57.3%; Score 33.8; DB 3; Length 918;
Best Local Similarity 84.4%; Pred. No. 0.18;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 15 TTATGGTATGGTGGTATGATGTTTCAGTCTTTCGCTGATCAG 59
Db 912 TCACATAAGTGATGGTATGGTATGATGTTTCAGATCTTTCGCTGATCAG 868

RESULT 14
US-09-782-397-15
Sequence 15, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Mafti, Pradip K.
Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-782-397-15

Query Match 57.3%; Score 33.8; DB 3; Length 918;
Best Local Similarity 84.4%; Pred. No. 0.18;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 15 TTATGGTATGGTGGTATGATGTTTCAGTCTTTCGCTGATCAG 59
Db 7 TCACATAAGTGATGGTATGGTATGATGTTTCAGATCTTTCGCTGATCAG 51

RESULT 15
US-10-651-453-13/c
Sequence 13, Application US/10651453
Publication No. US20040091484A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Mafti, Pradip K.
Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS,
NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROP

Fri May 19 11:37:24 2006

us-09-211-691-6.түрбм

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1  TITLE OF INVENTION:  DETECTION OF CANCERS
2  FILE REFERENCE:  316082000103
3  CURRENT APPLICATION NUMBER:  US/10/651,453
4  CURRENT FILING DATE:  2003-08-29
5  PRIOR APPLICATION NUMBER:  US 09/782,397
6  PRIOR FILING DATE:  2001-02-13
7  PRIOR APPLICATION NUMBER:  US 08/862,124
8  PRIOR FILING DATE:  1997-05-22
9  PRIOR APPLICATION NUMBER:  US 08/657,449
10 PRIOR FILING DATE:  1996-05-22
11 NUMBER OF SEQ ID NOS:  29
12 SOFTWARE:  PatentIn version 3.1
13 SEQ ID NO. 13
14 LENGTH:  918
15 TYPE:  DNA
16 ORGANISM:  Homo Sapiens
17 FEATURE:
18 NAME/KEY:  CDS
19 LOCATION:  (1)..(906)
20 OTHER INFORMATION:
21 FEATURE:
22 NAME/KEY:  CDS
23 LOCATION:  (913)..(918)
24 OTHER INFORMATION:
25 US-10-651-453-13

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Query Match	57.3%;	Score 33.8;	DB 8;	Length 918;
Best Local Similarity	84.4%;	Pred. No. 0.18;		
Matches 38;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY 15 TTAGTGTGATGGTGATGGTCAGGCTCTTCGCGTATCAG 59
 | | | | | | | | | | | | | | | | | |
Db 912 TCACATATGATGGTGATGGTCAGATCTTCTTCGCGTATCAG 868

Search completed: May 19, 2006, 05:02:08
Job time : 1016.91 secs

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RESULT 10
US-11-075-891-15/c
; Sequence 15, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; FILE REFERENCE: 263922US96
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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